

SQANTI3 report

Unique Genes: 61030

Unique Isoforms: 82279

Transcript Classification

Category	Isoforms, count
FSM	11384
ISM	18317
NIC	3118
NNC	35
Genic Genomic	3612
Antisense	4320
Fusion	68
Intergenic	9524
Genic Intron	31901

Gene Classification

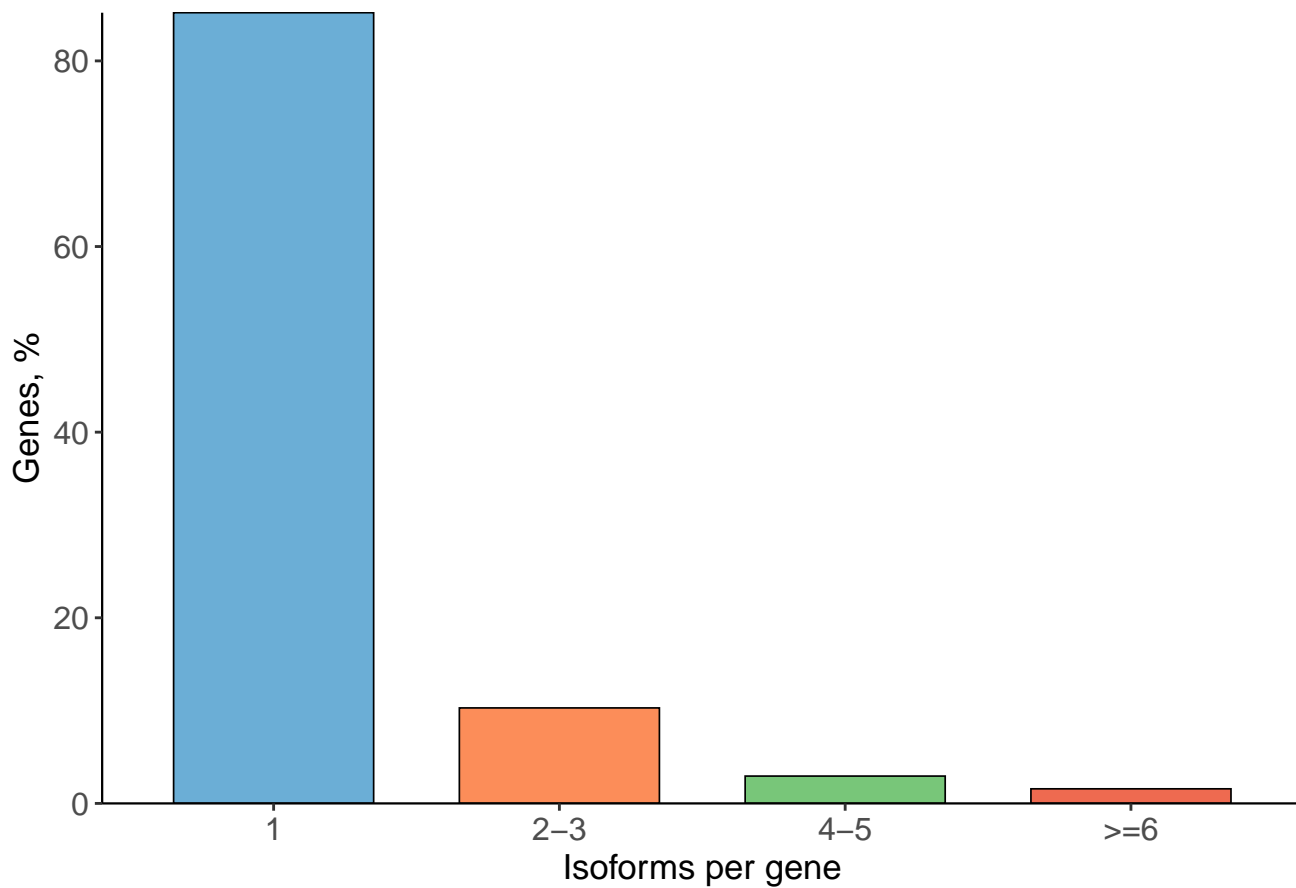
Category	Genes, count
Annotated Genes	16208
Novel Genes	44822

Splice Junction Classification

Category	SJs, count	Percent
Known canonical	60976	93.96
Known Non–canonical	2263	3.49
Novel canonical	1529	2.36
Novel Non–canonical	130	0.20

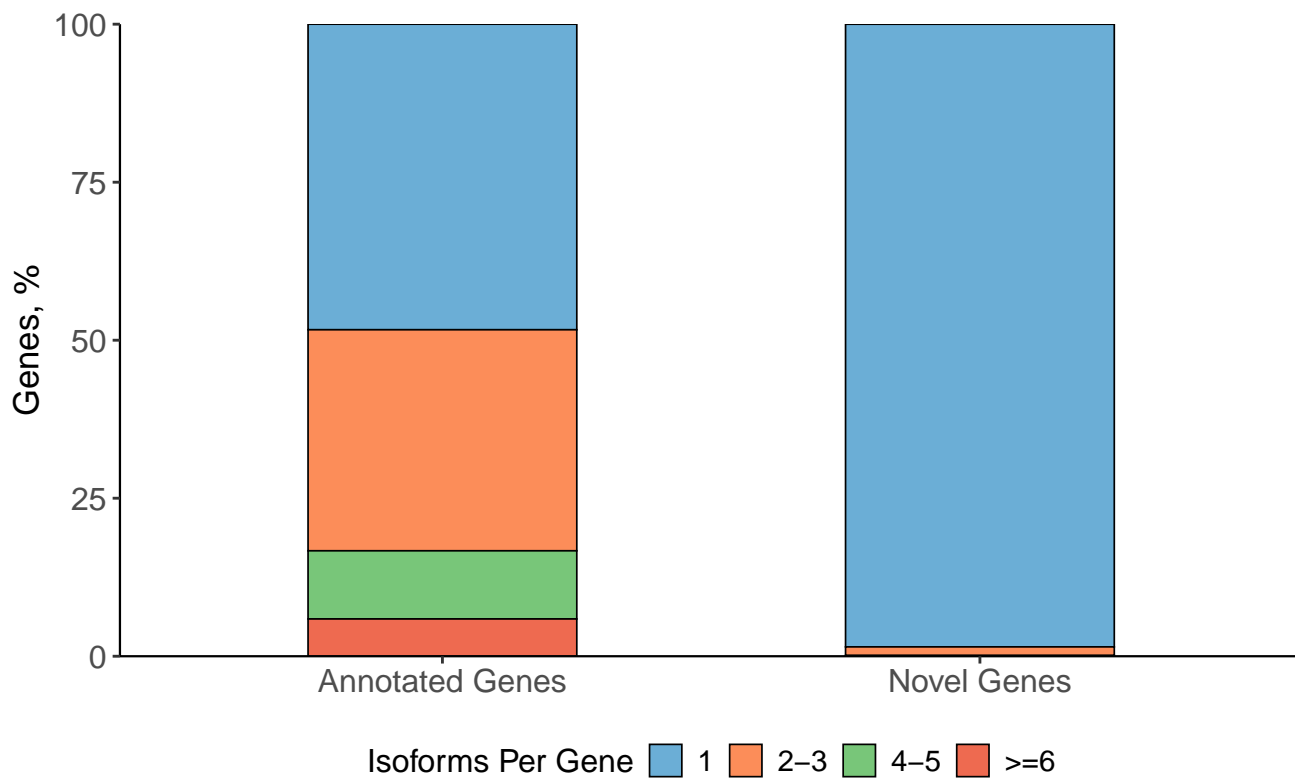
Gene Characterization

Number of Isoforms per Gene

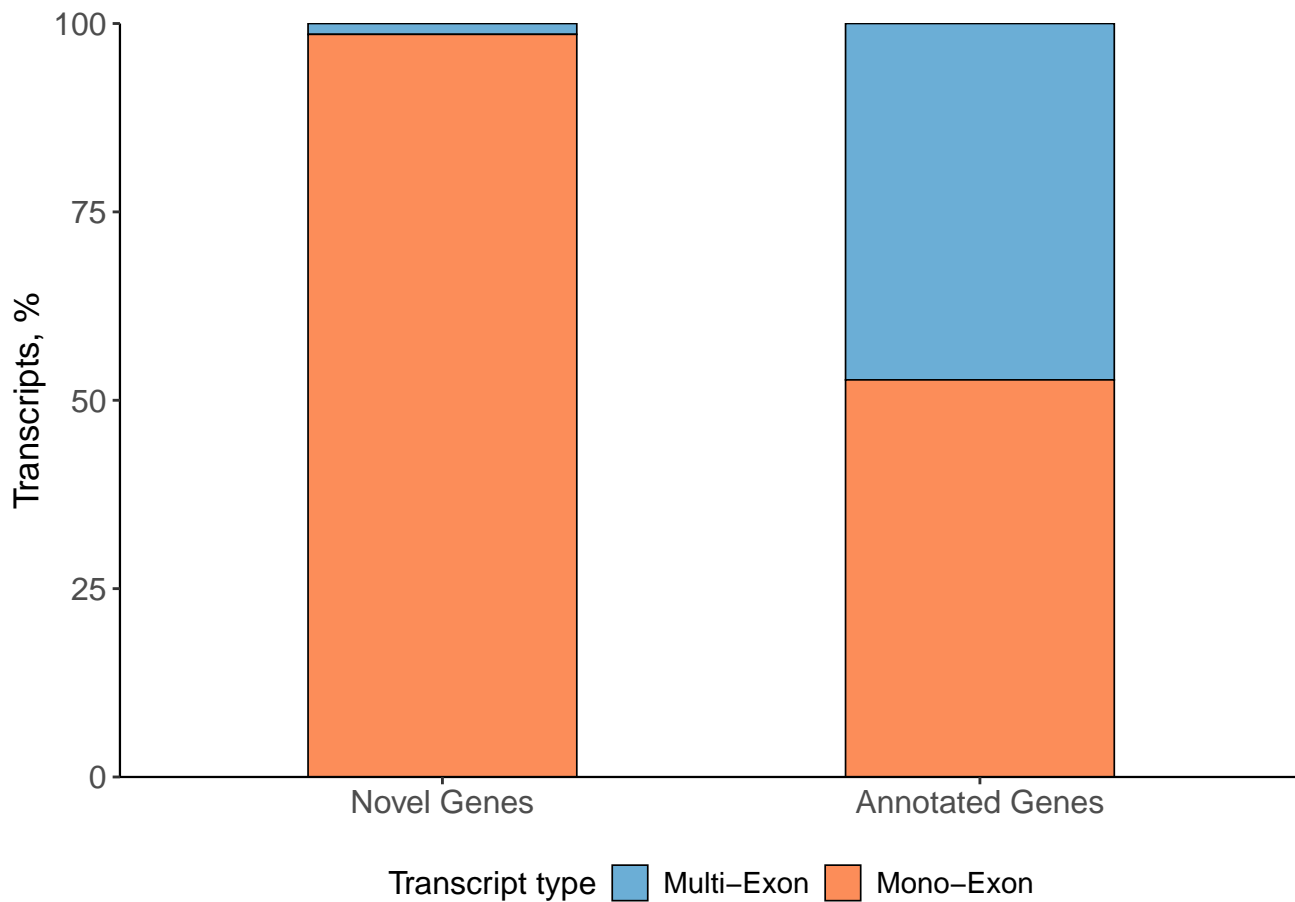


Number of Isoforms per Gene

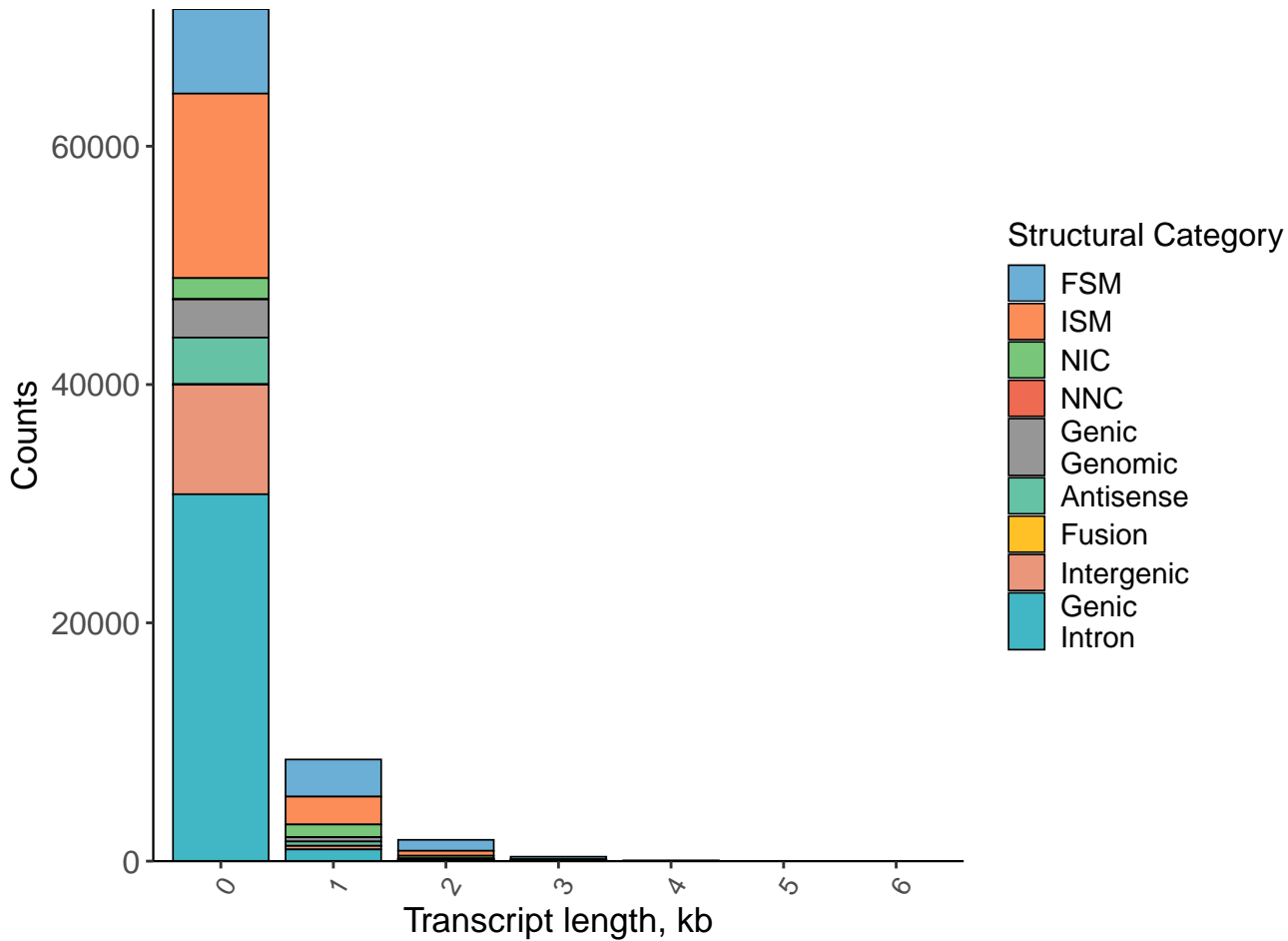
Known vs Novel Genes



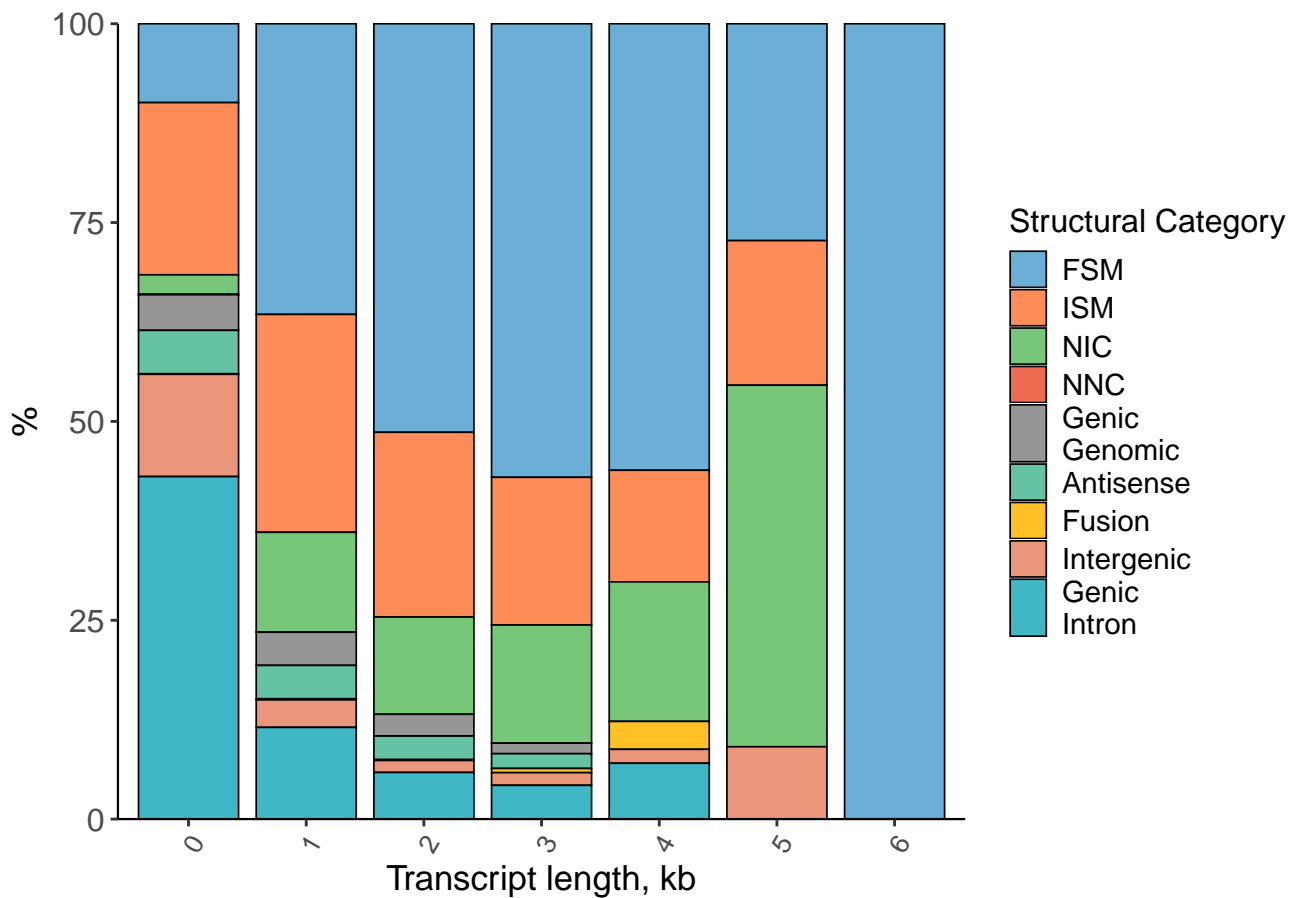
Distribution of Mono- vs Multi-Exon Transcripts



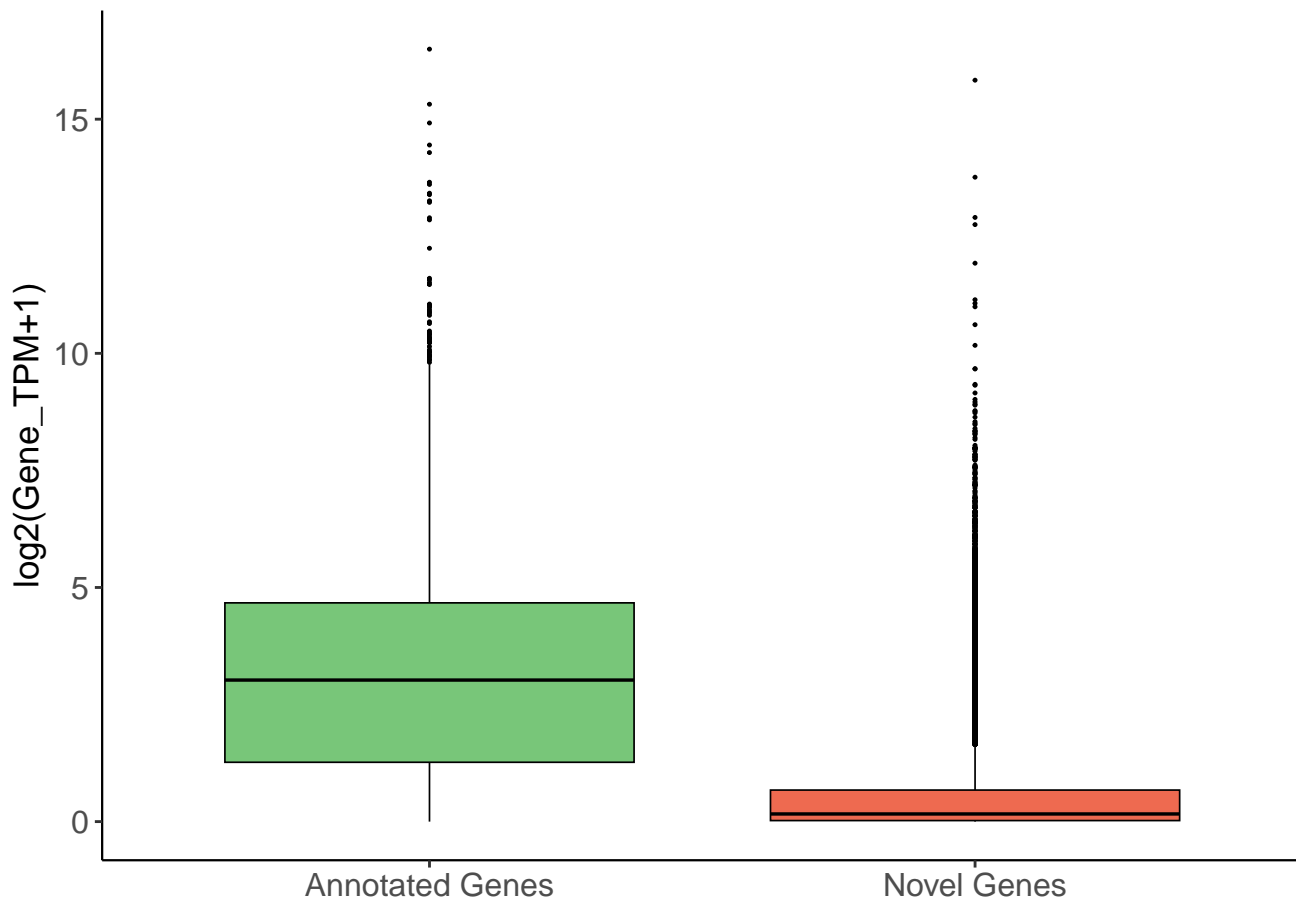
Structural Categories by Transcript Length



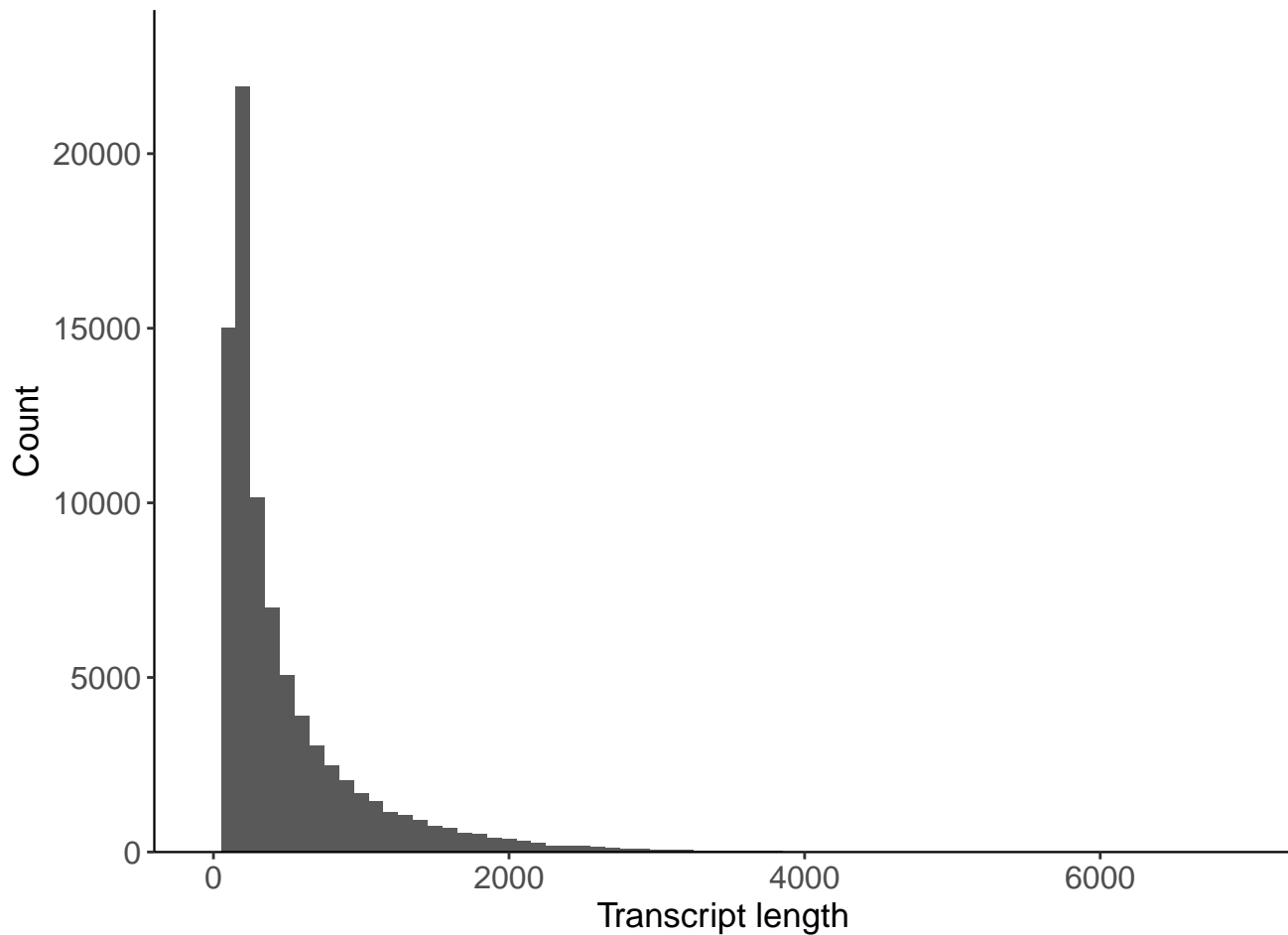
Structural Categories by Transcript Length



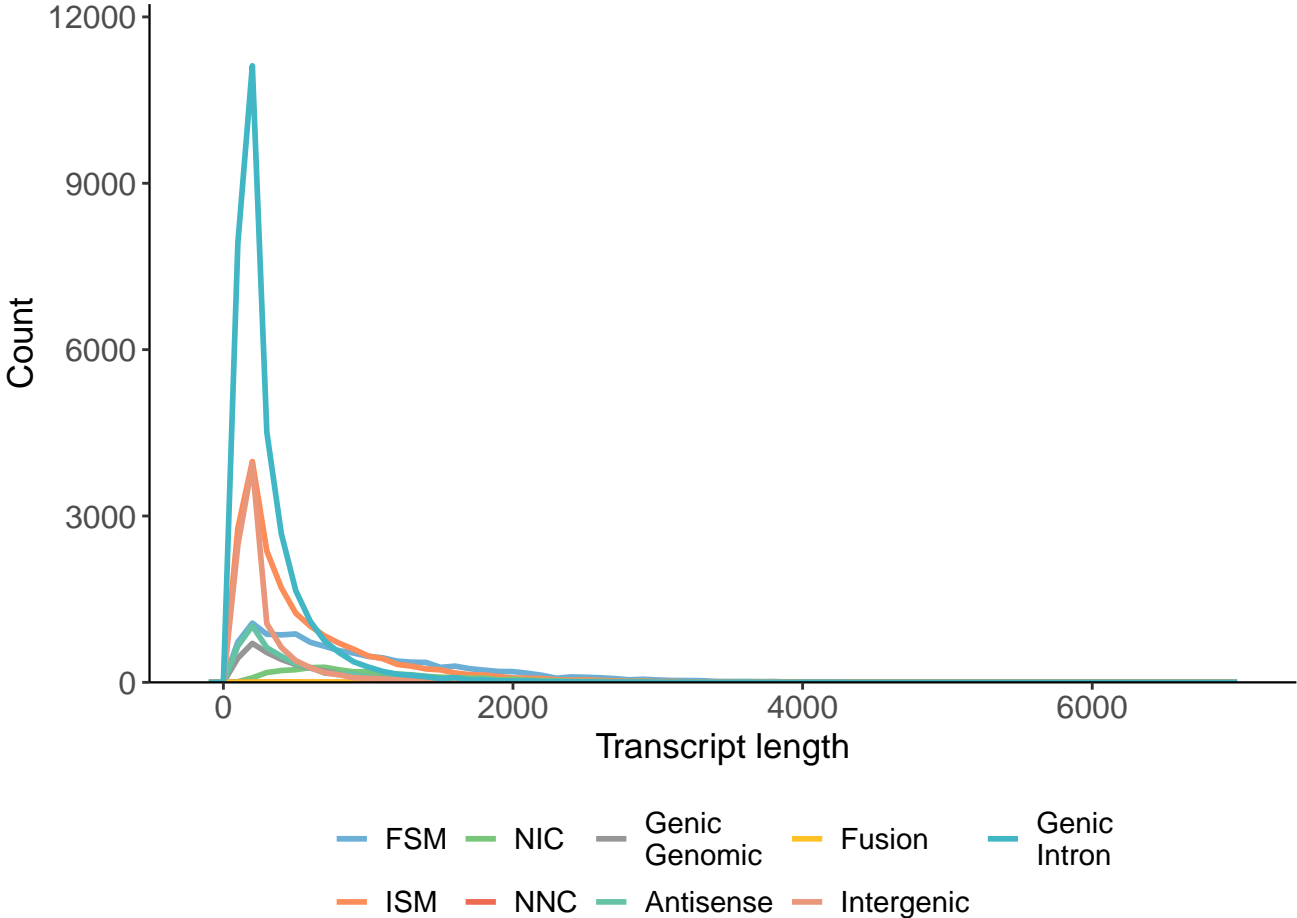
Annotated vs Novel Gene Expression



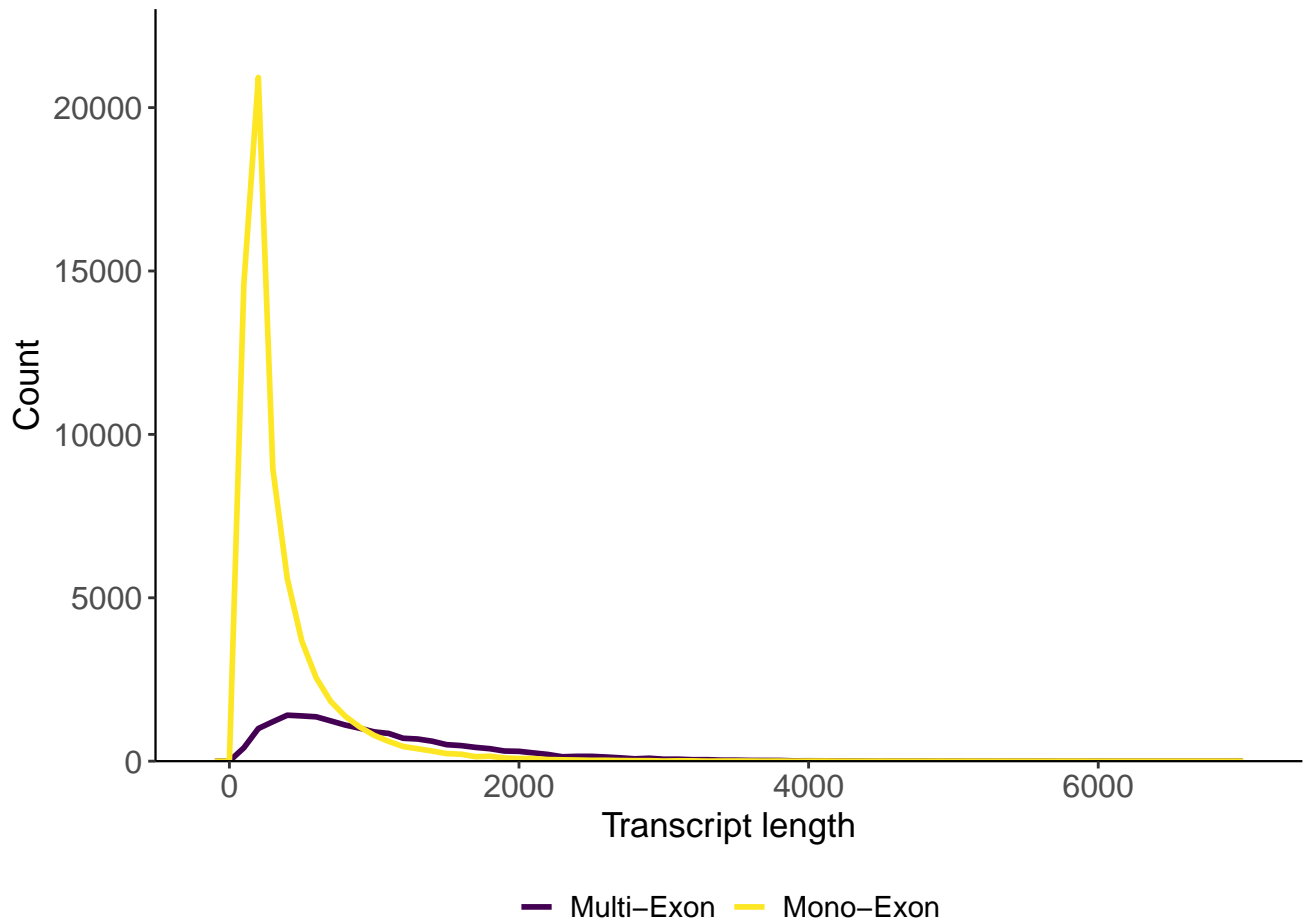
All Transcript Lengths Distribution



Transcript Lengths Distribution by Structural Category

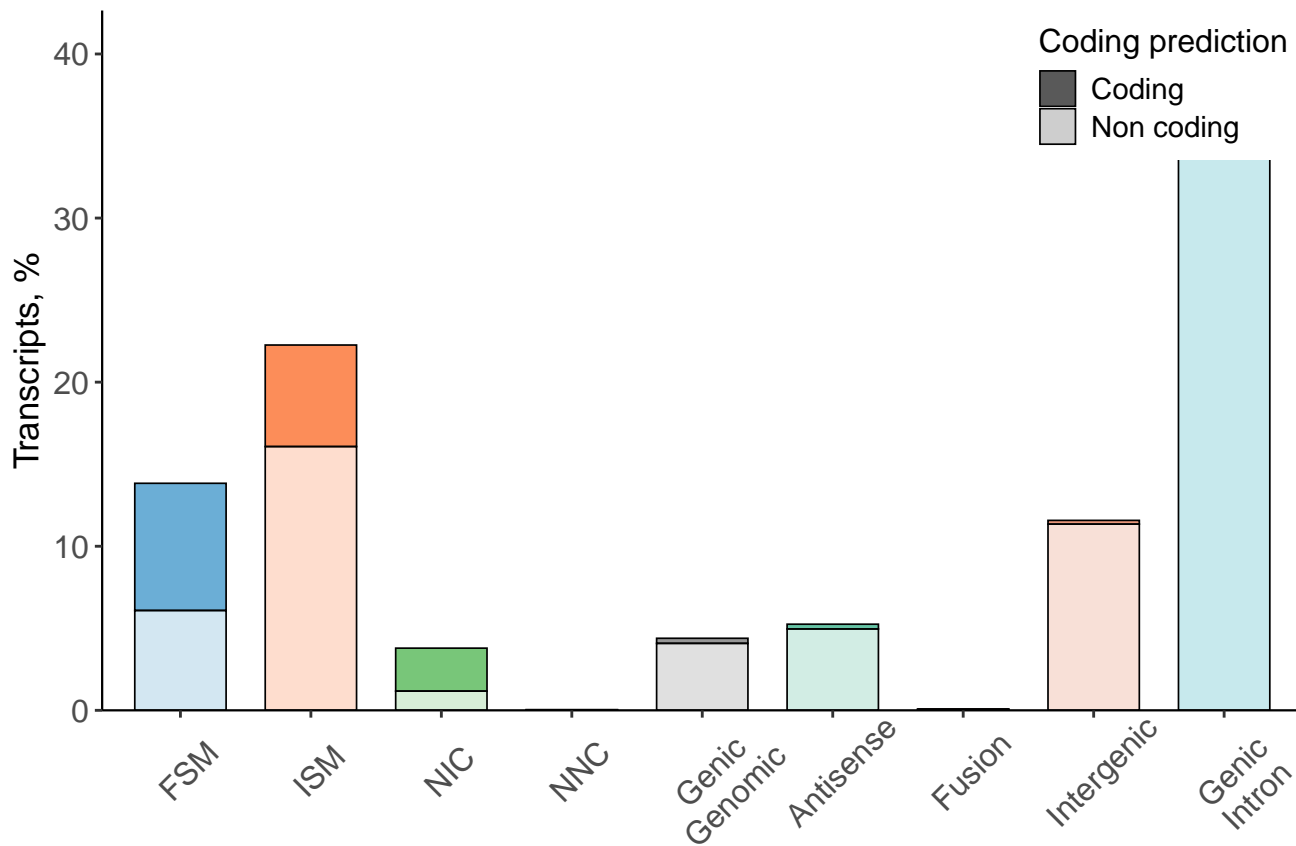


Mono- vs Multi- Exon Transcript Lengths Distribution

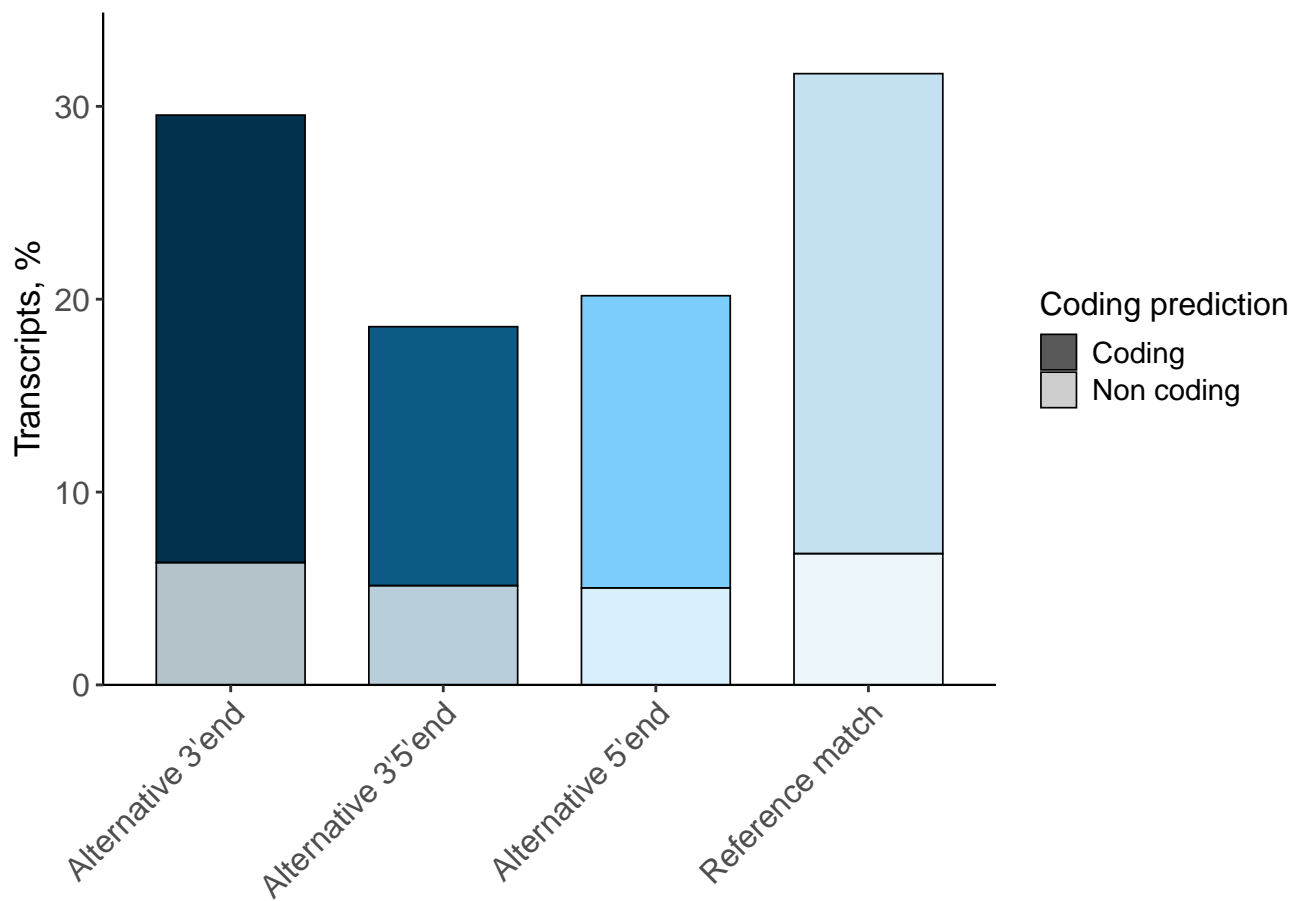


Structural Isoform Characterization

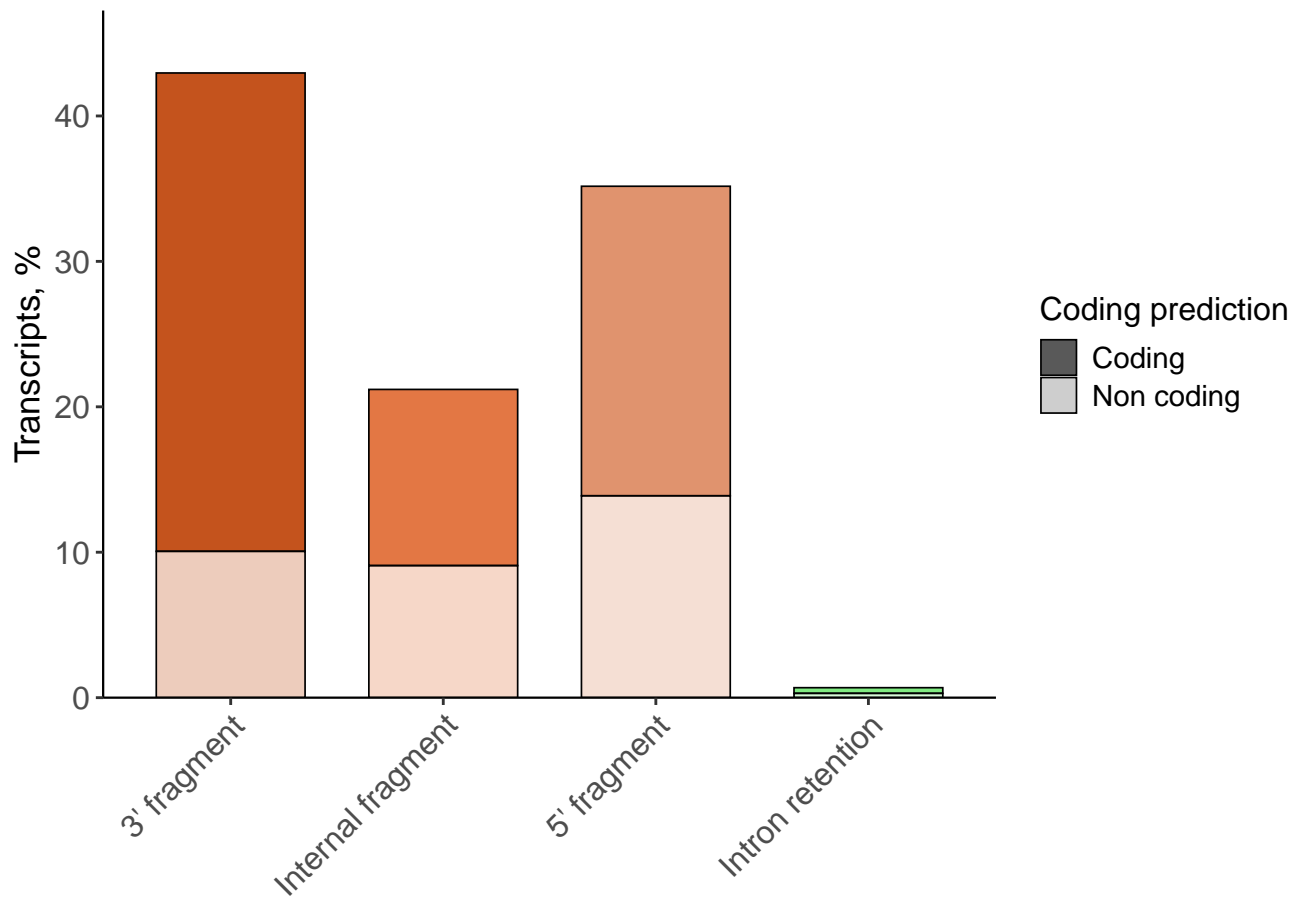
Isoform Distribution Across Structural Categories



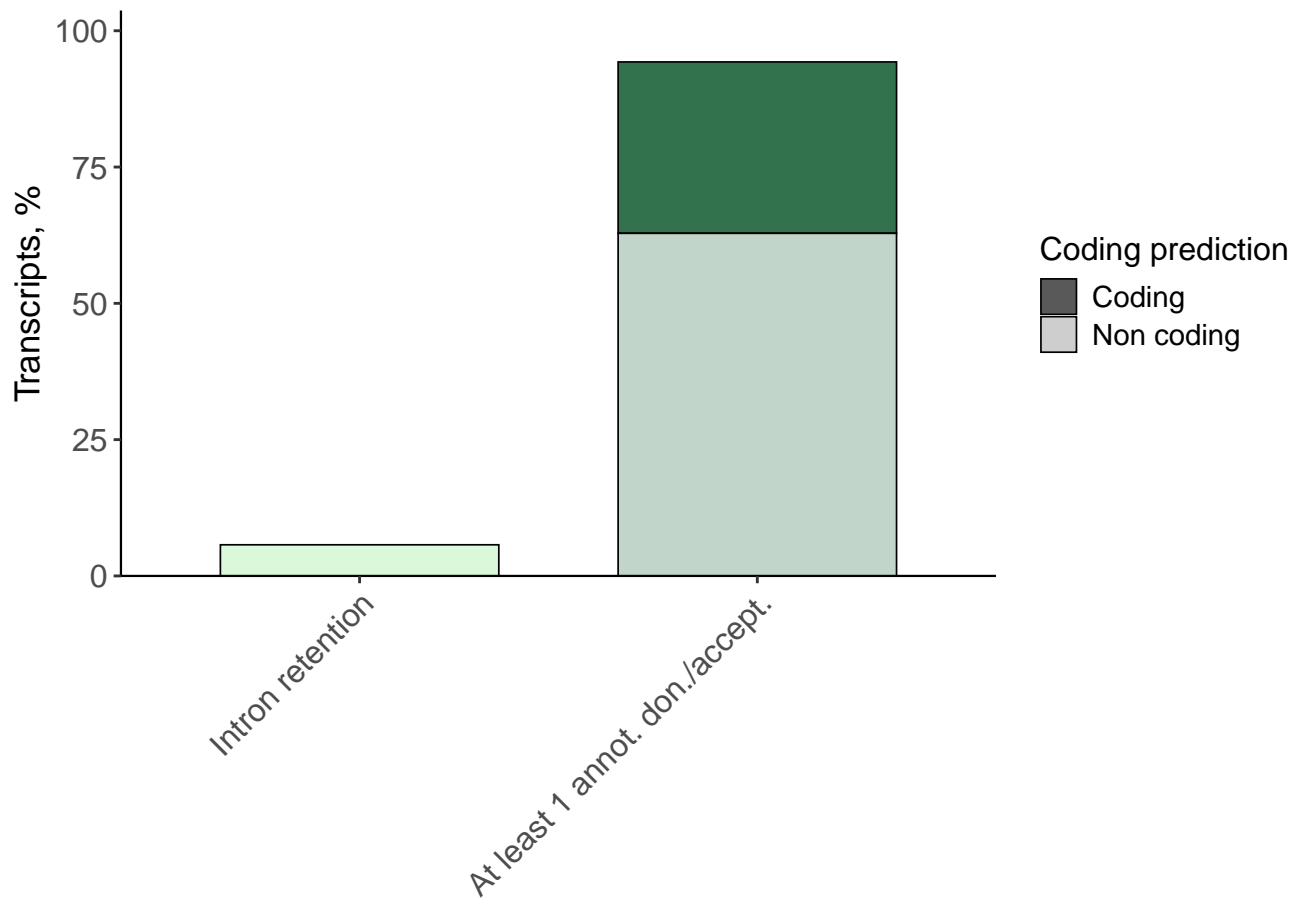
Isoform Distribution Across FSM



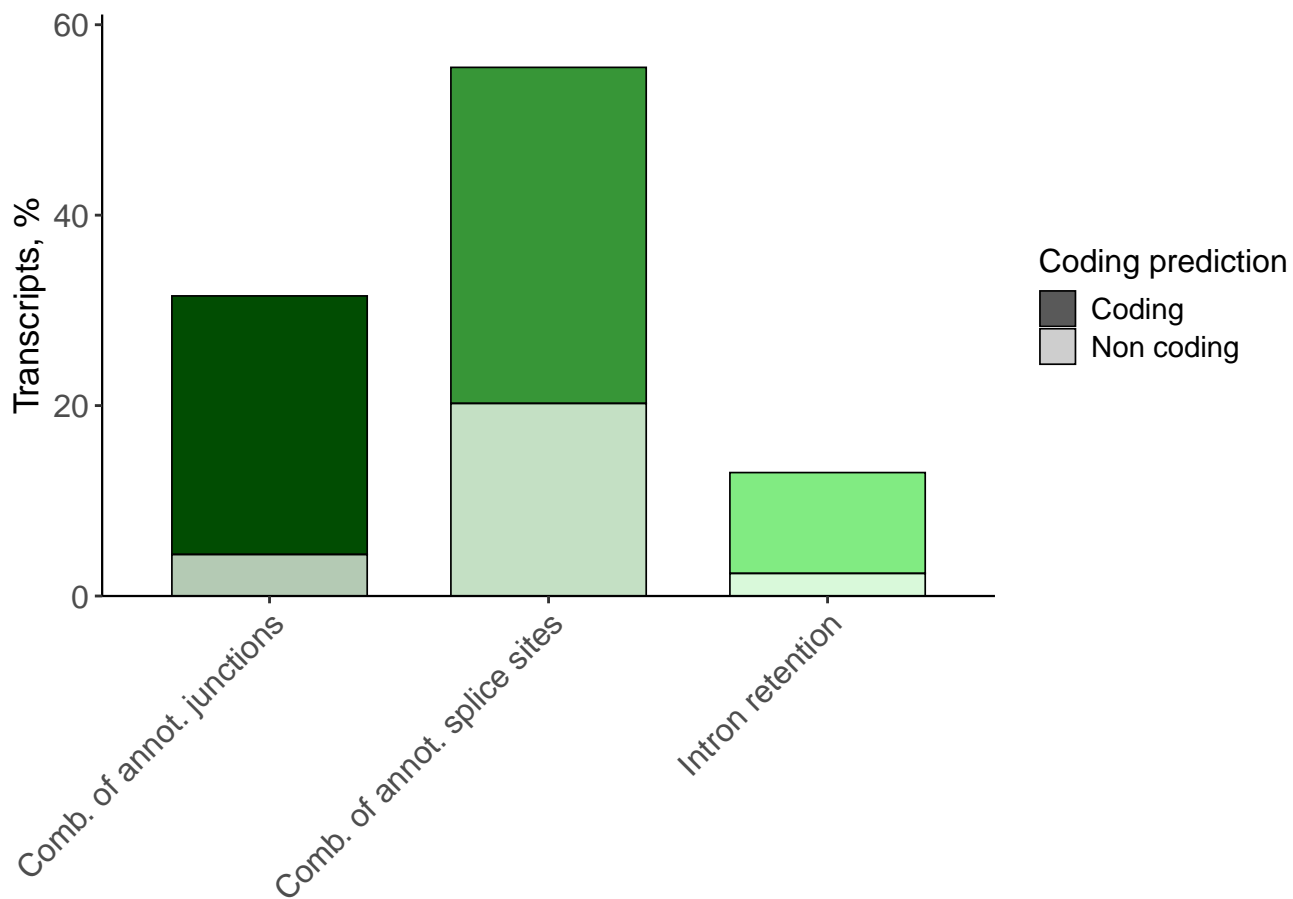
Isoform Distribution Across ISM



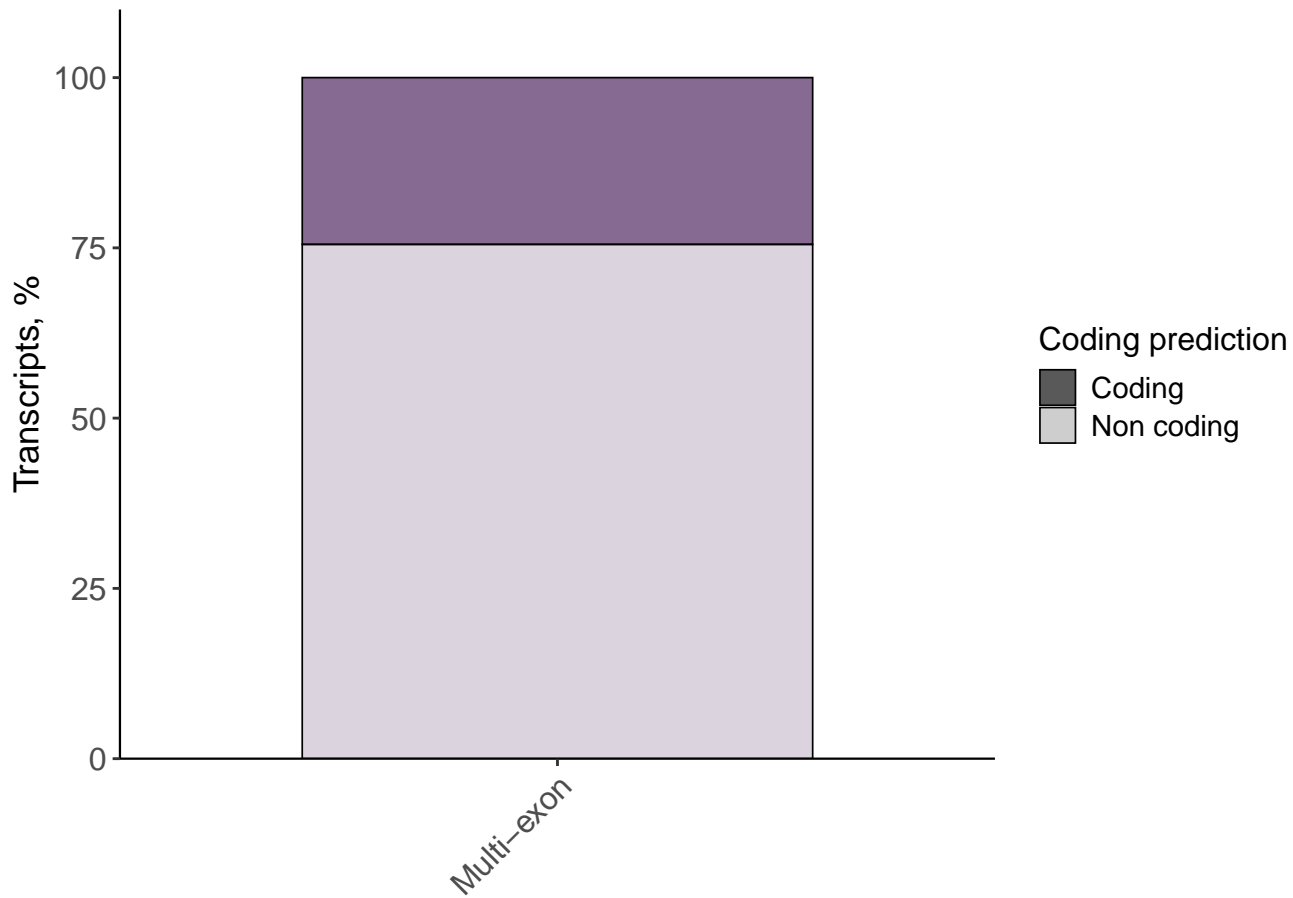
Isoform Distribution Across NNC



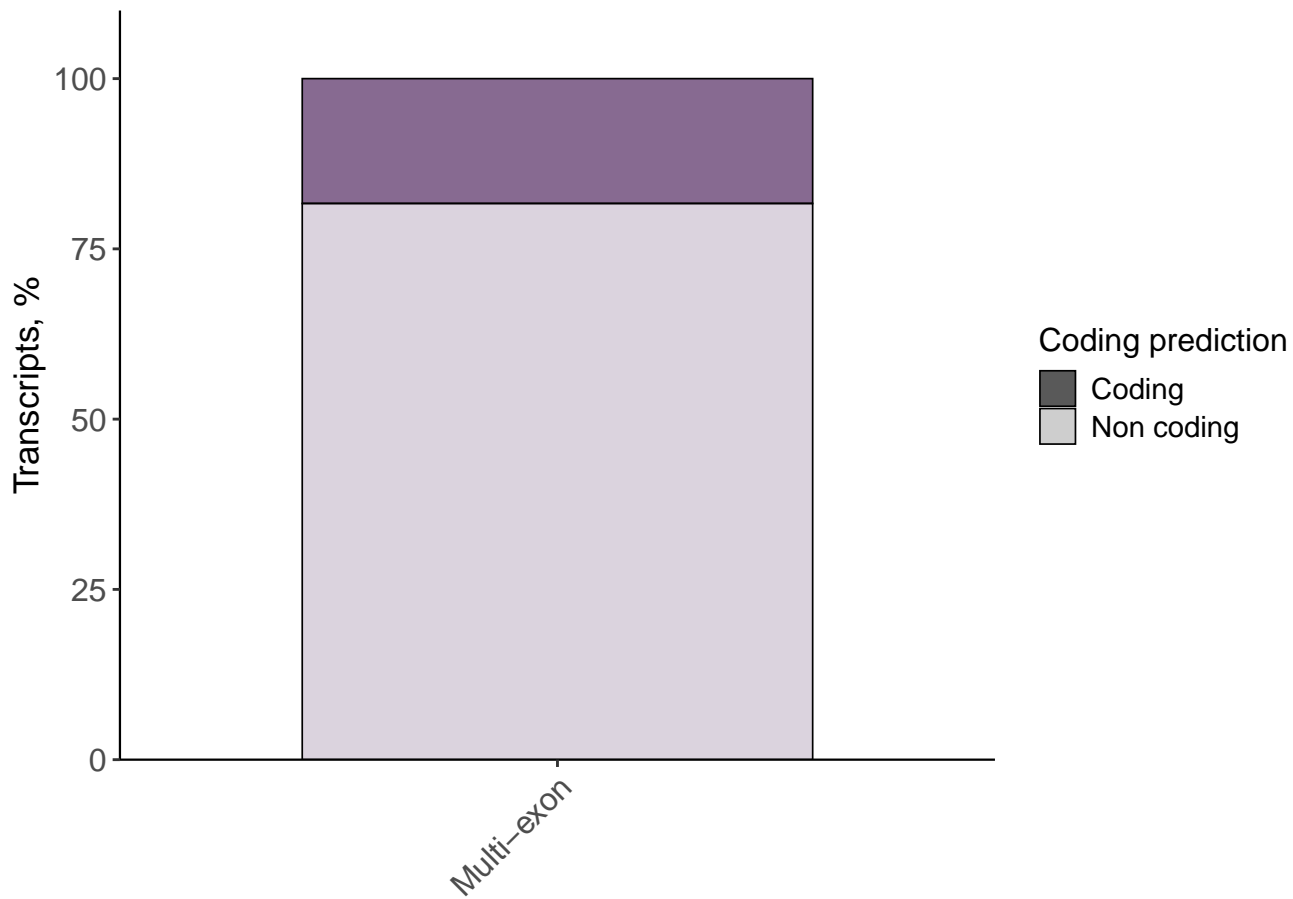
Isoform Distribution Across NIC



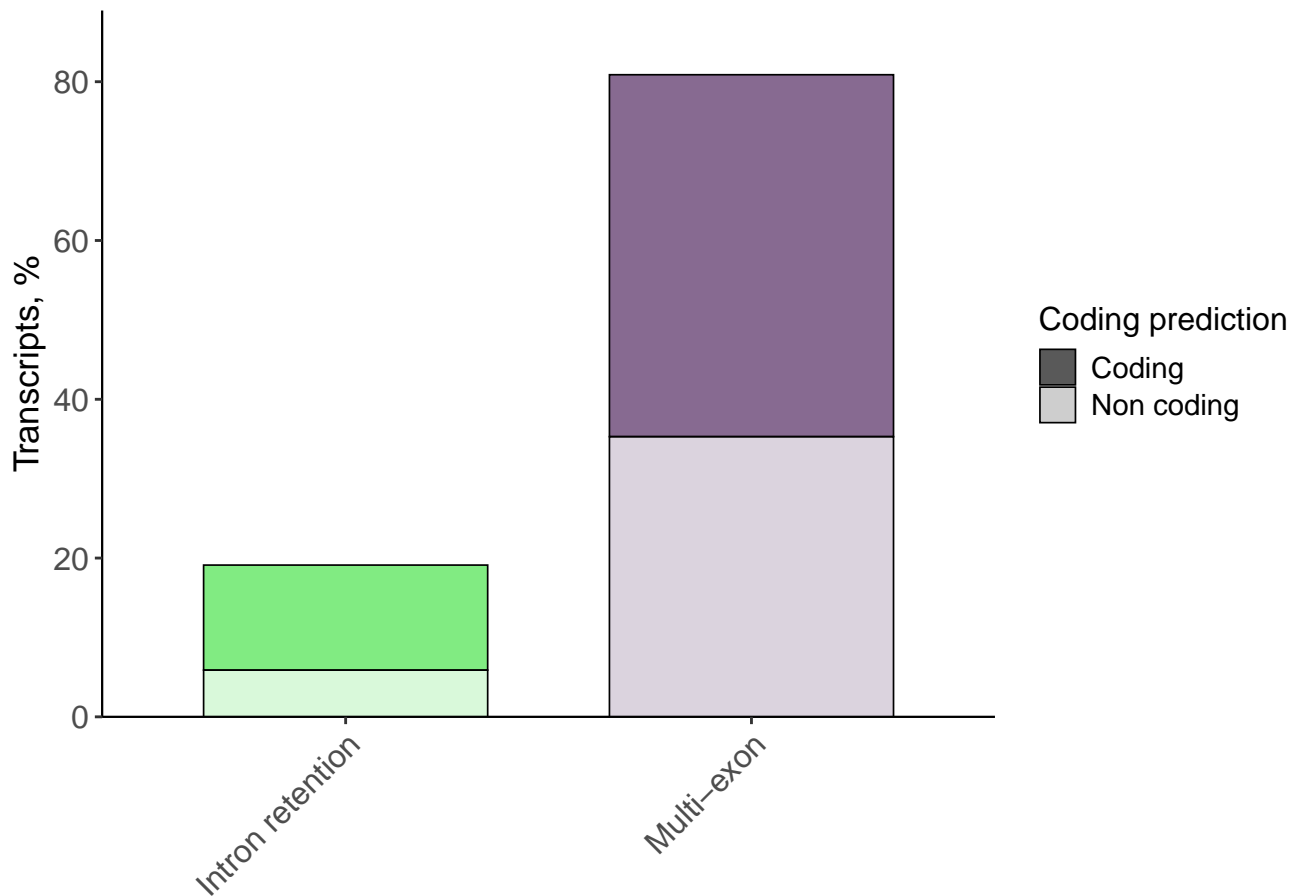
Isoform Distribution Across Genic Genomic



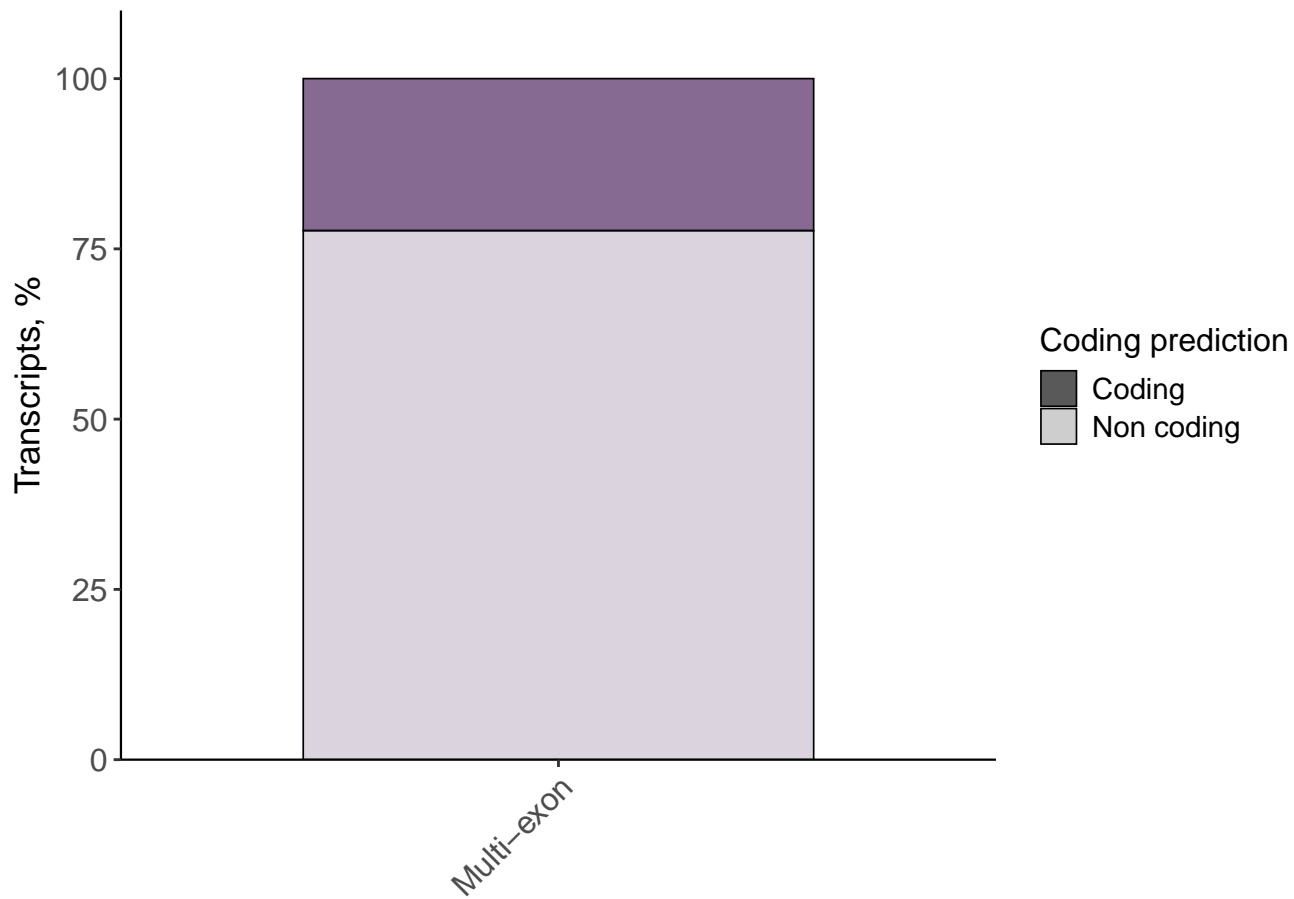
Isoform Distribution Across Antisense



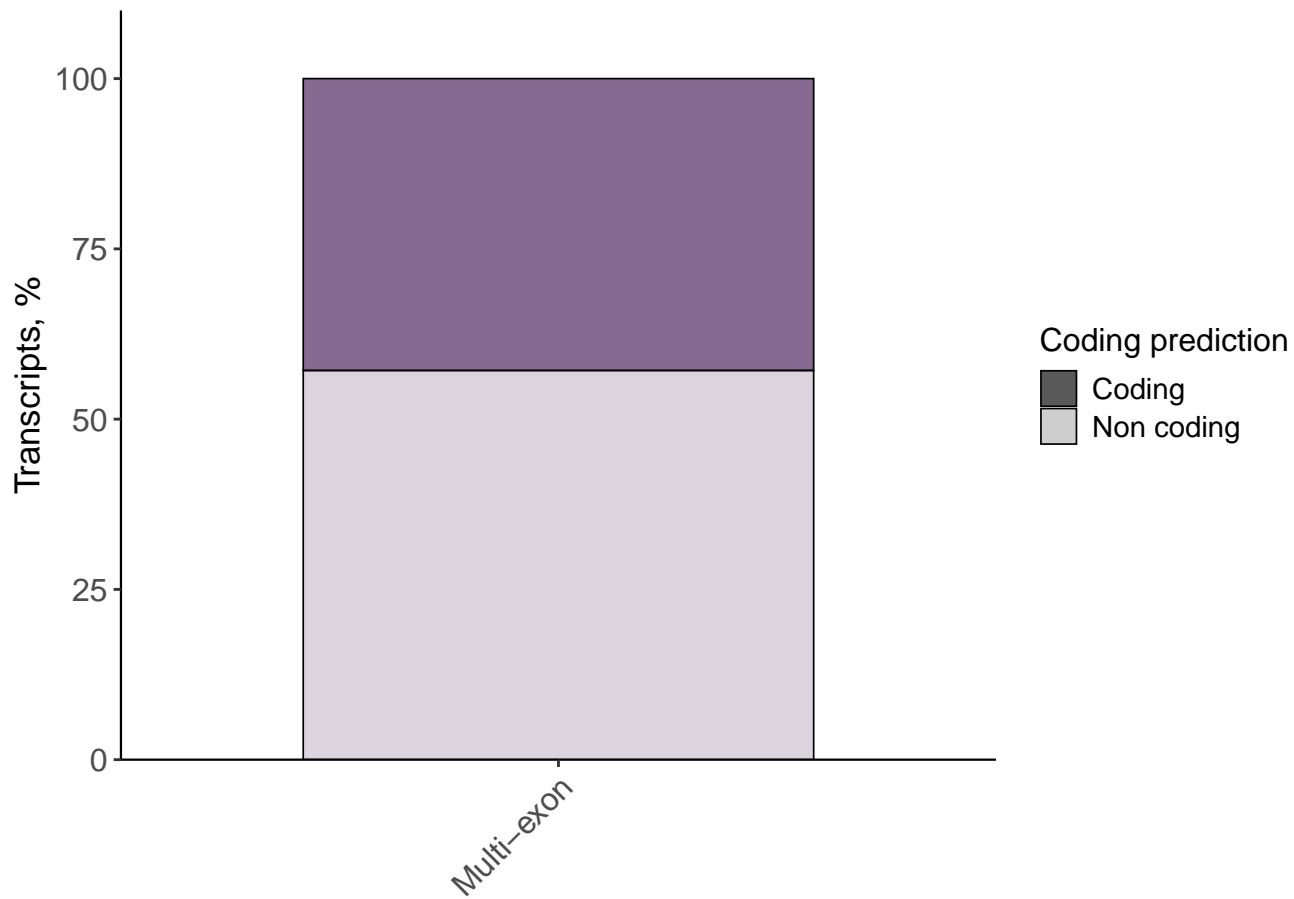
Isoform Distribution Across Fusion



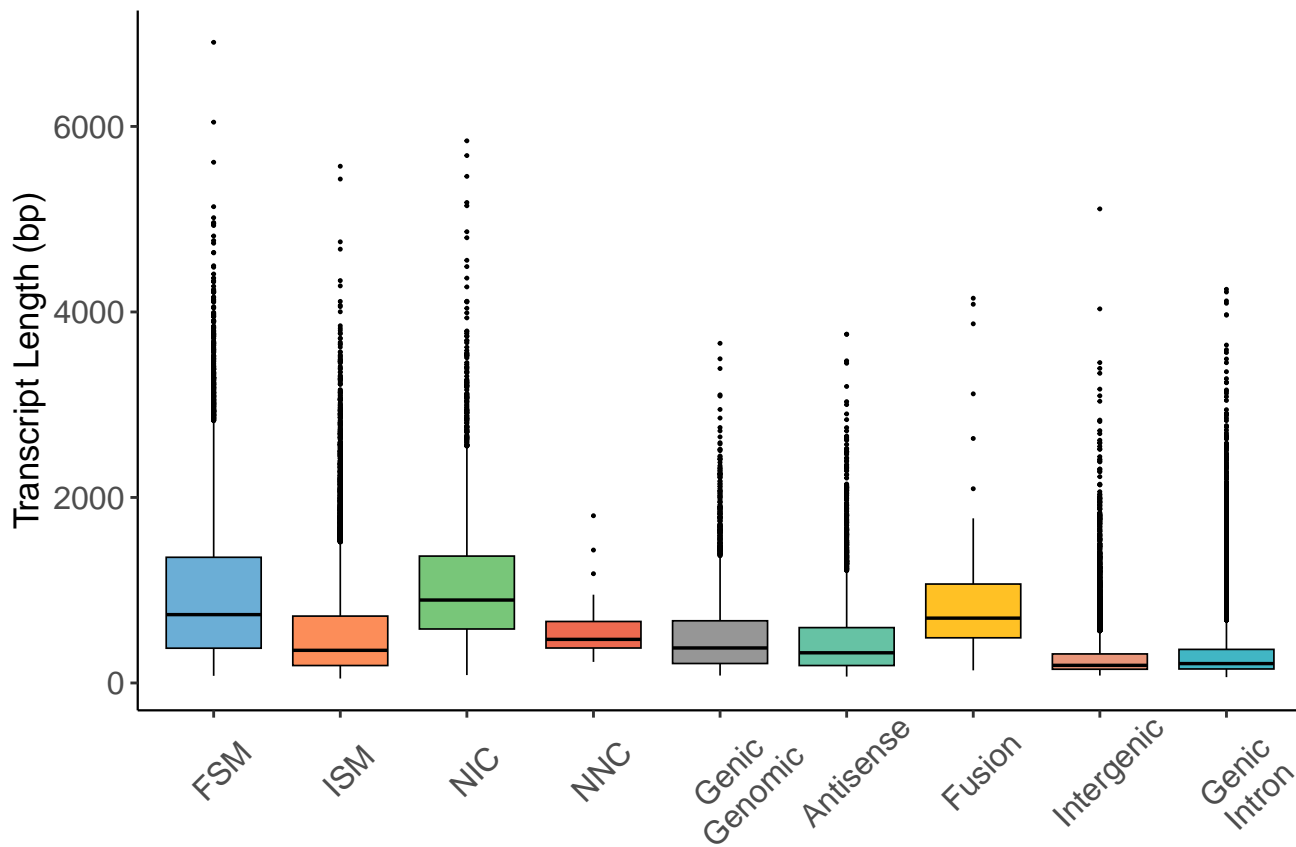
Isoform Distribution Across Intergenic



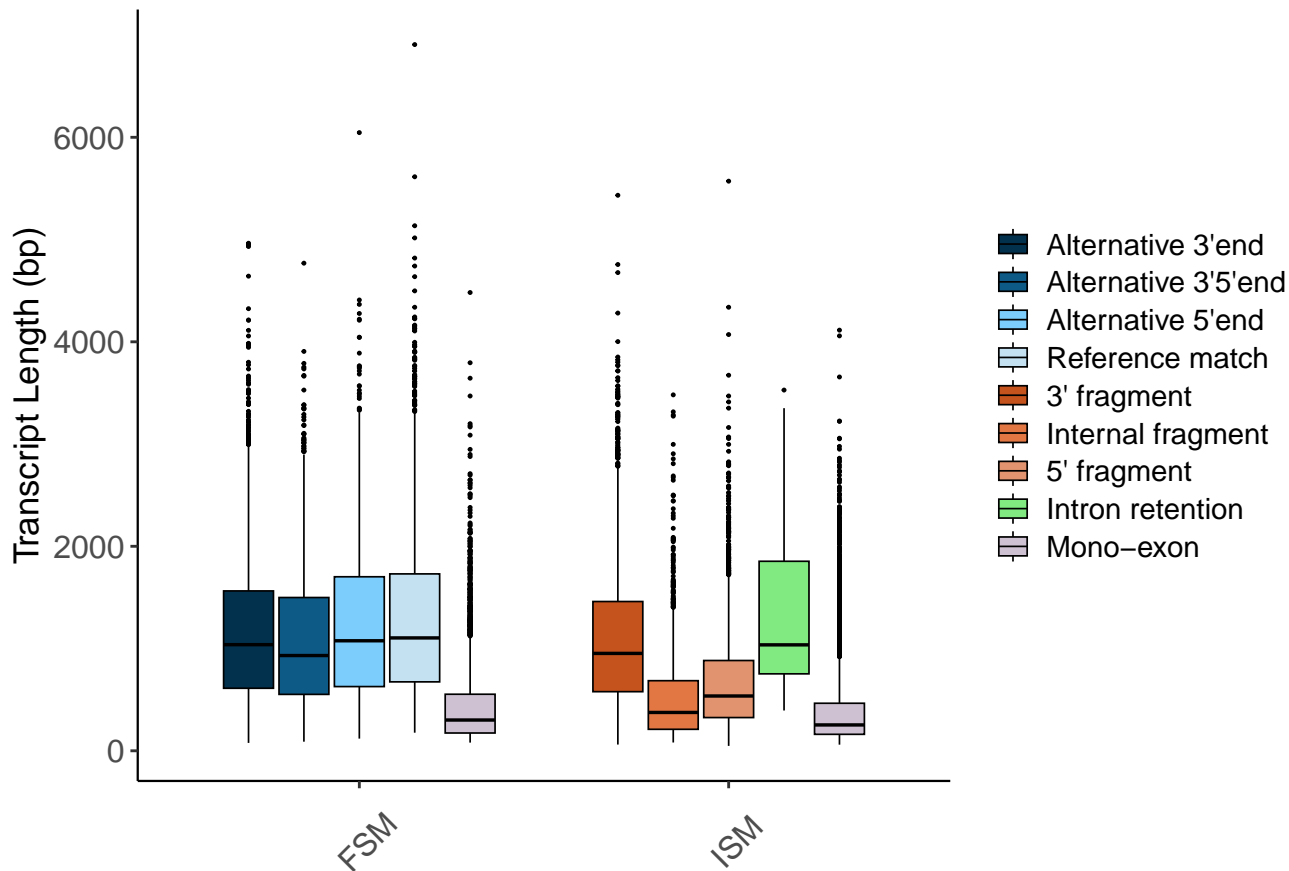
Isoform Distribution Across Genic Intron



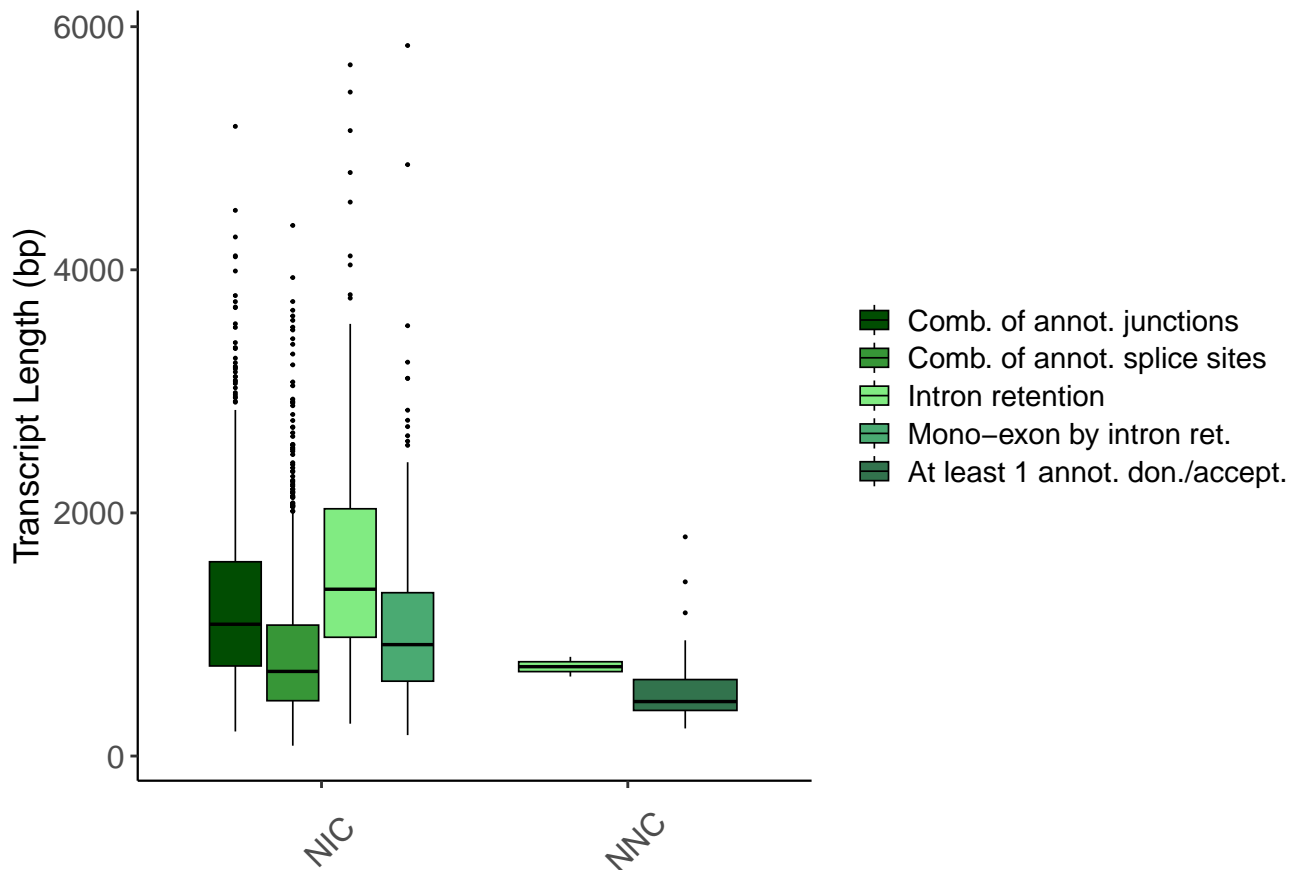
Transcript Lengths by Structural Classification



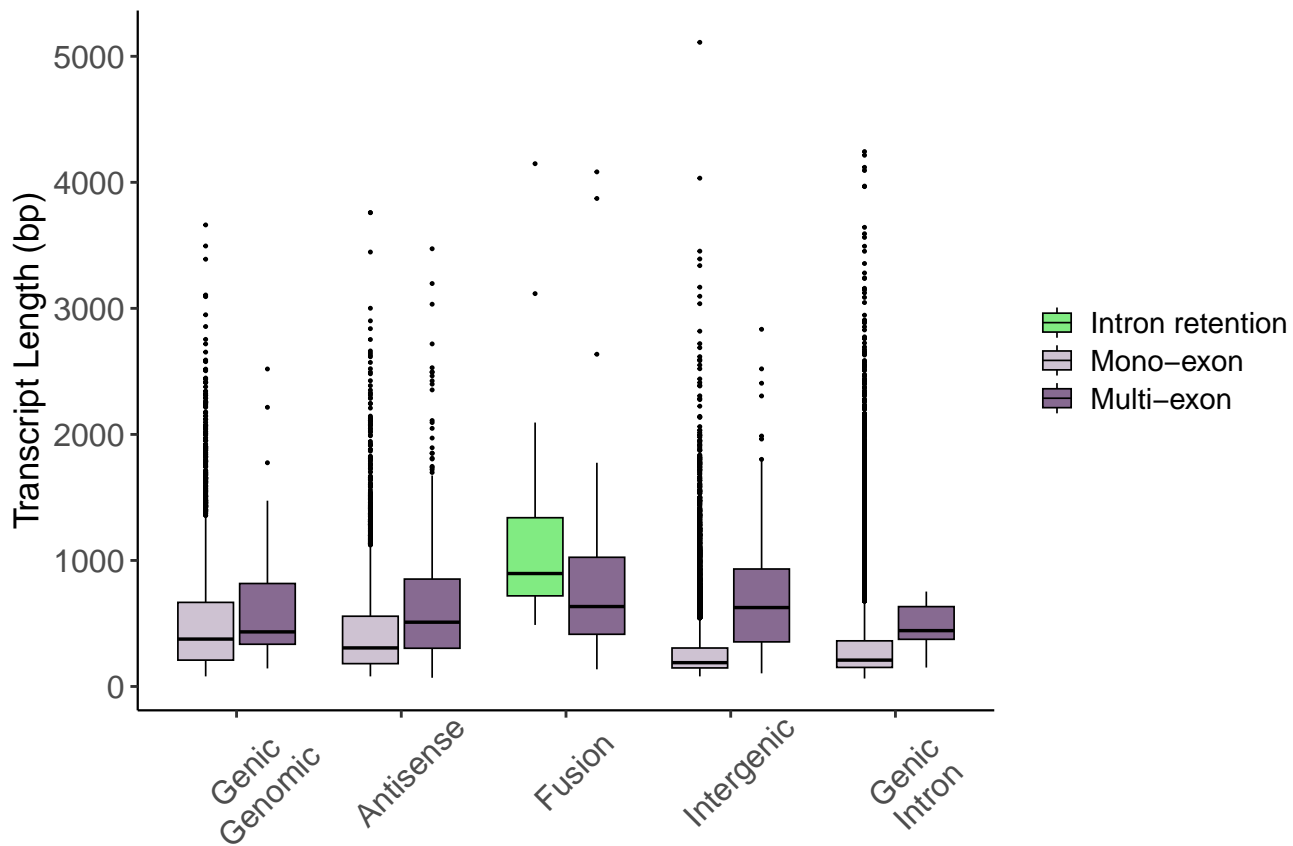
Transcript Lengths by Subcategory



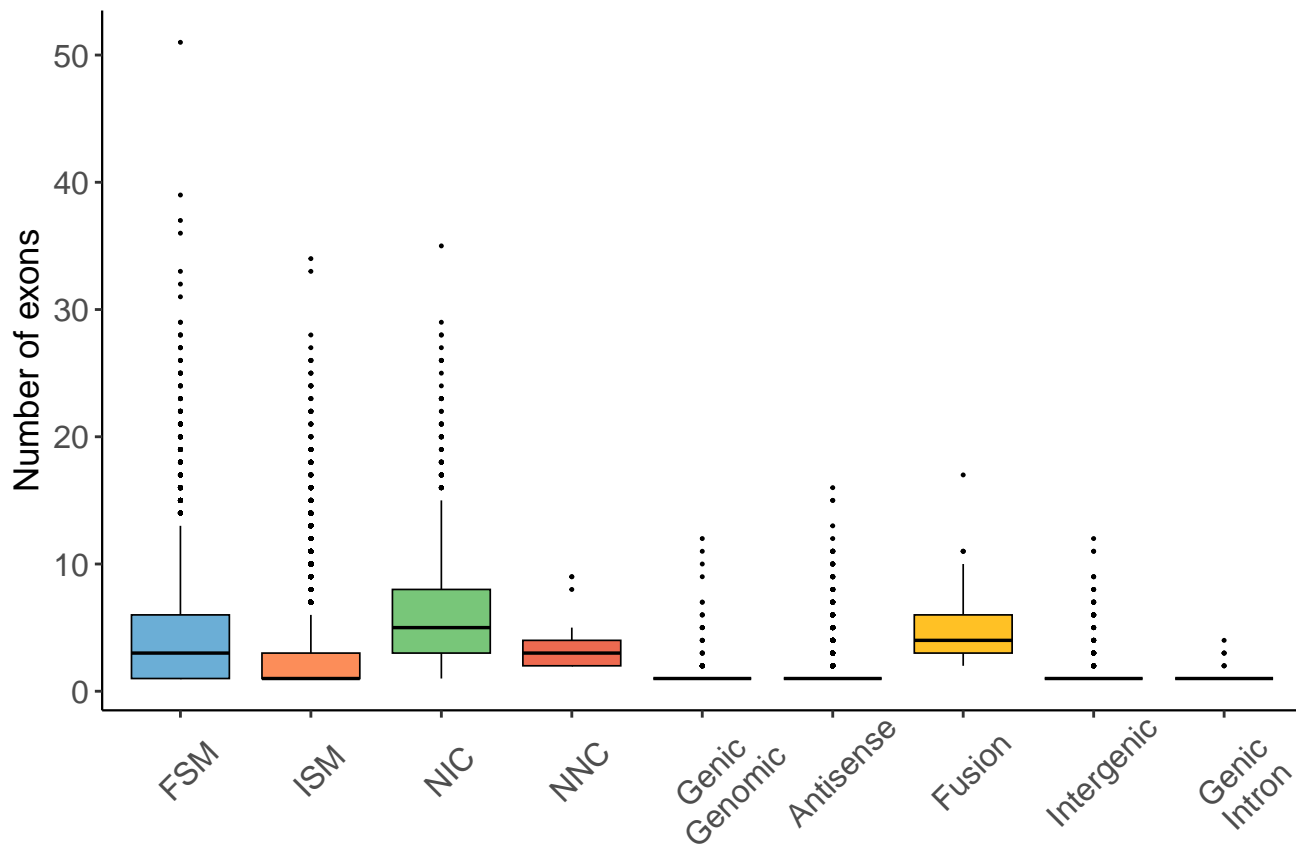
Transcript Lengths by Subcategory



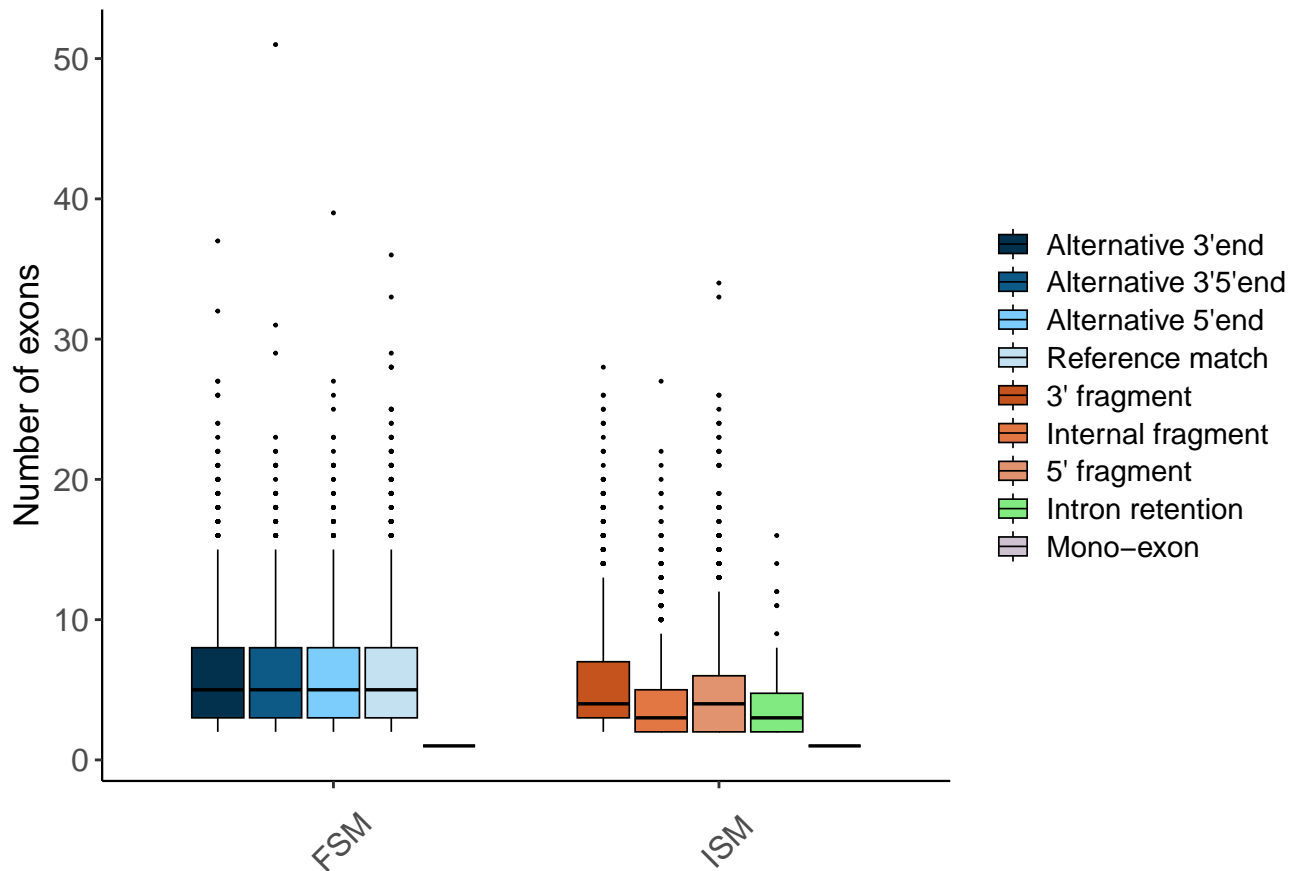
Transcript Lengths by Subcategory



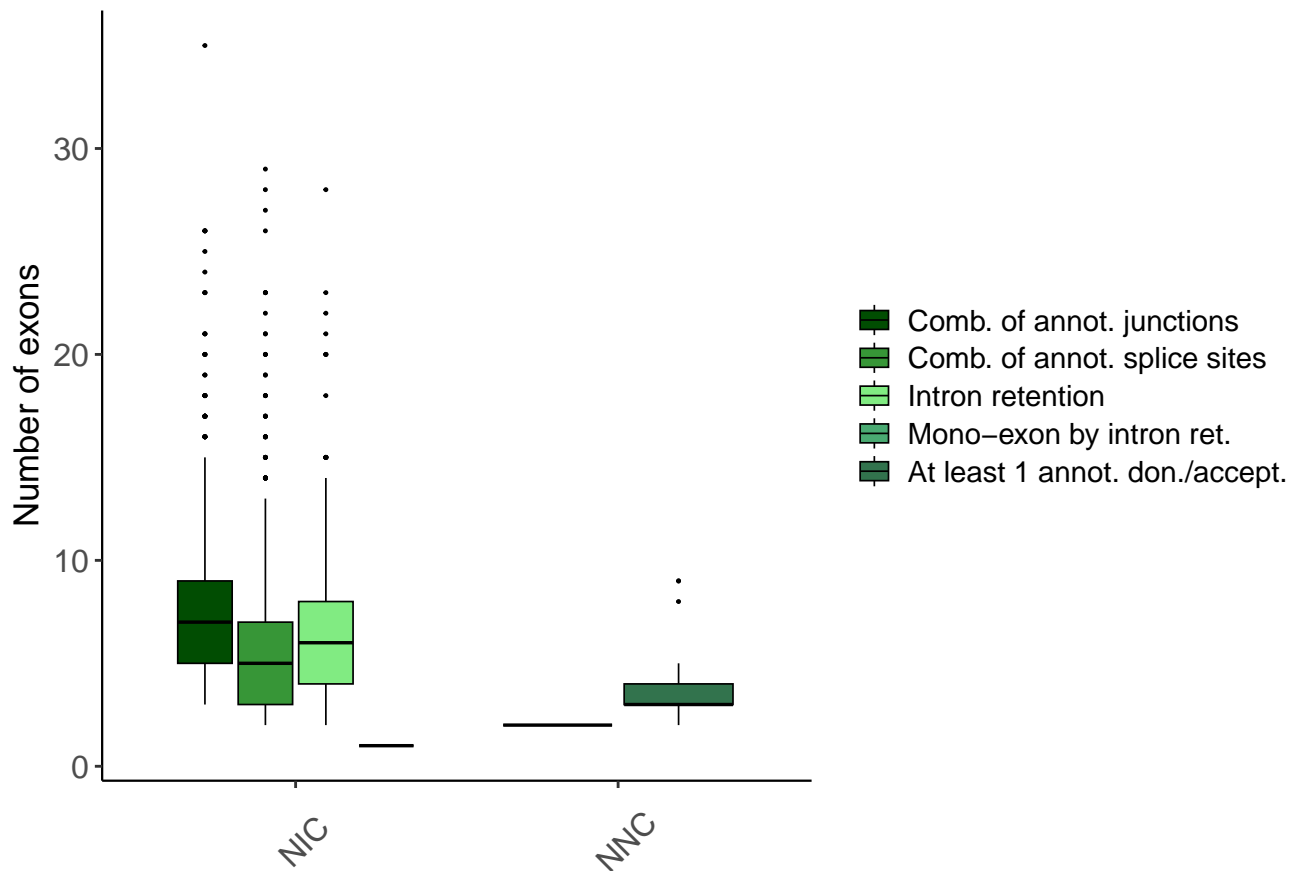
Exon Counts by Structural Classification



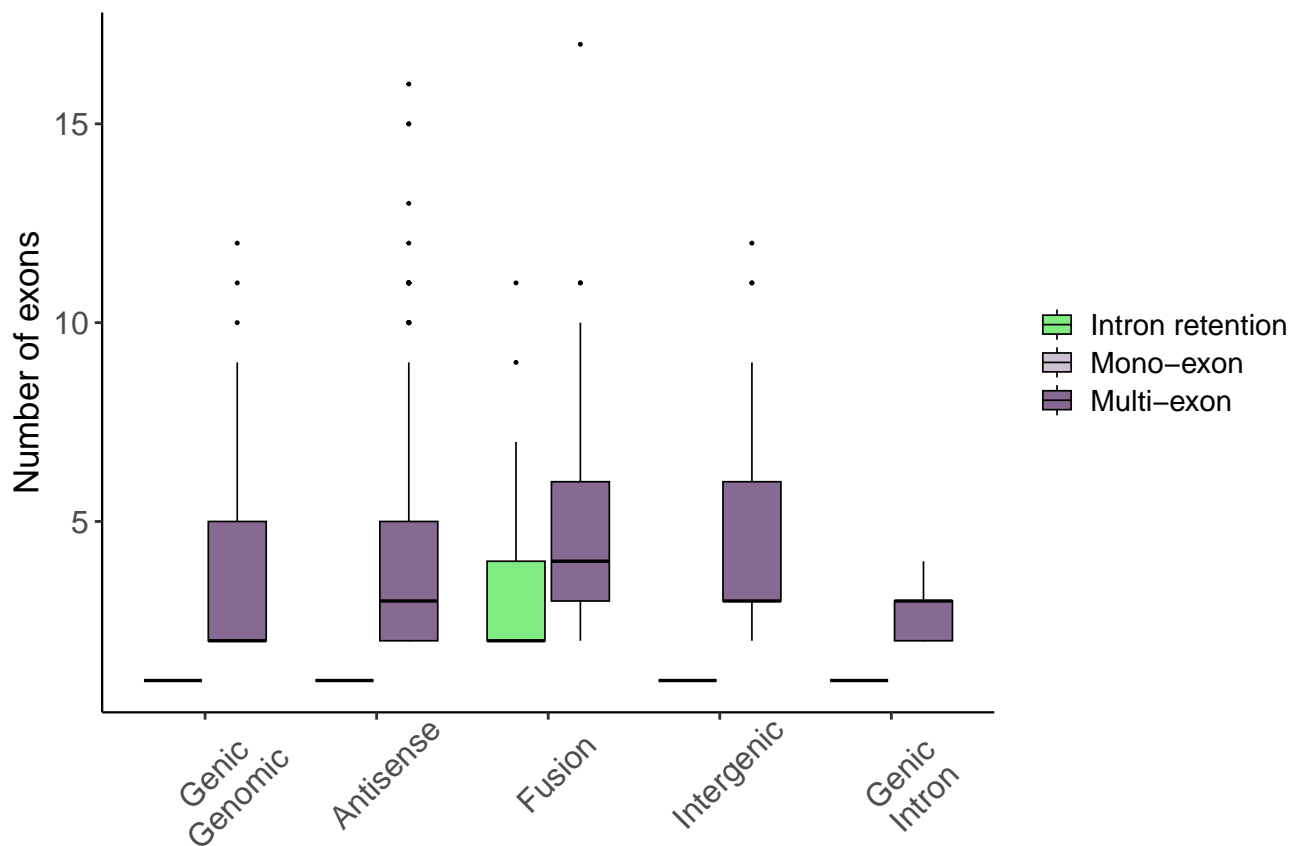
Exon Counts by Subcategory



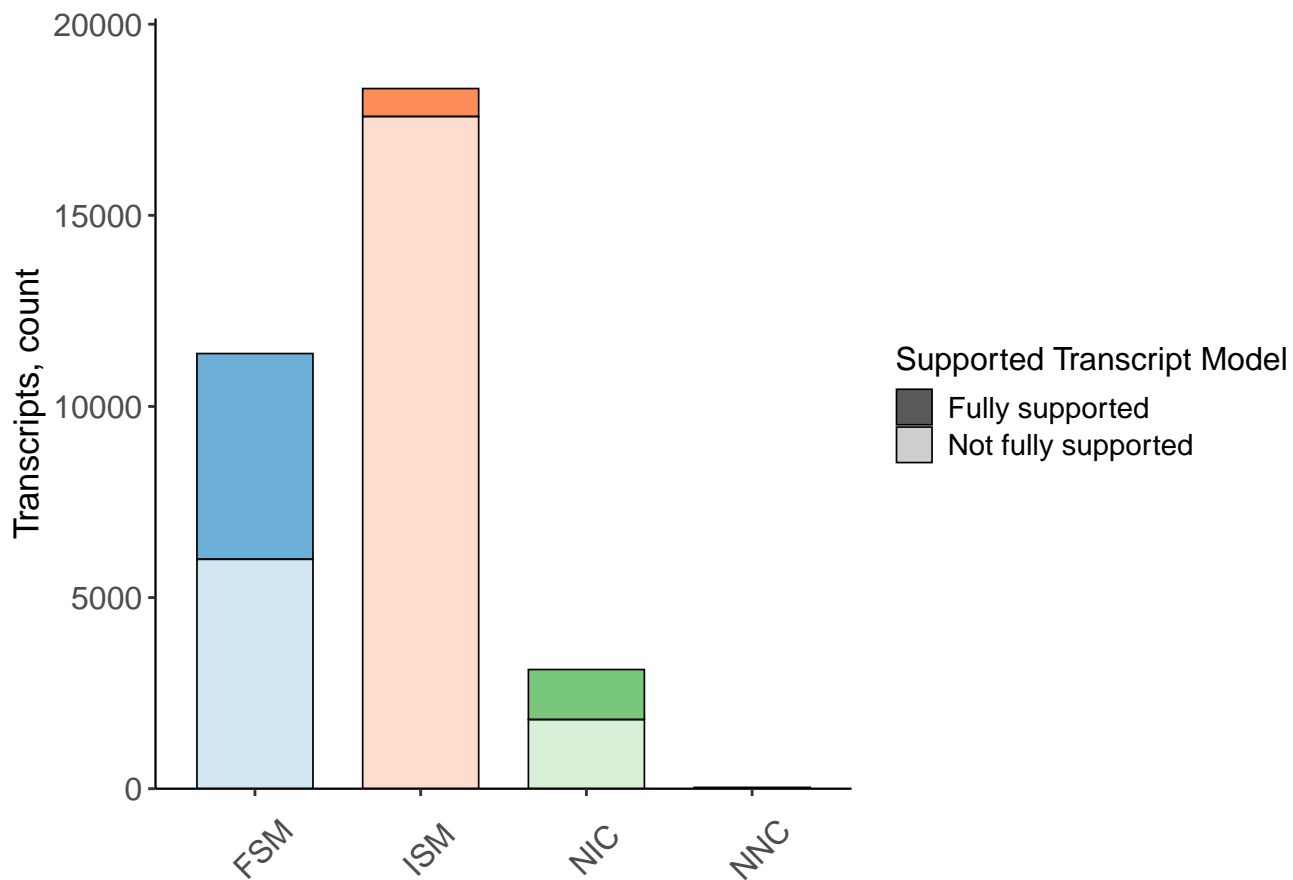
Exon Counts by Subcategory



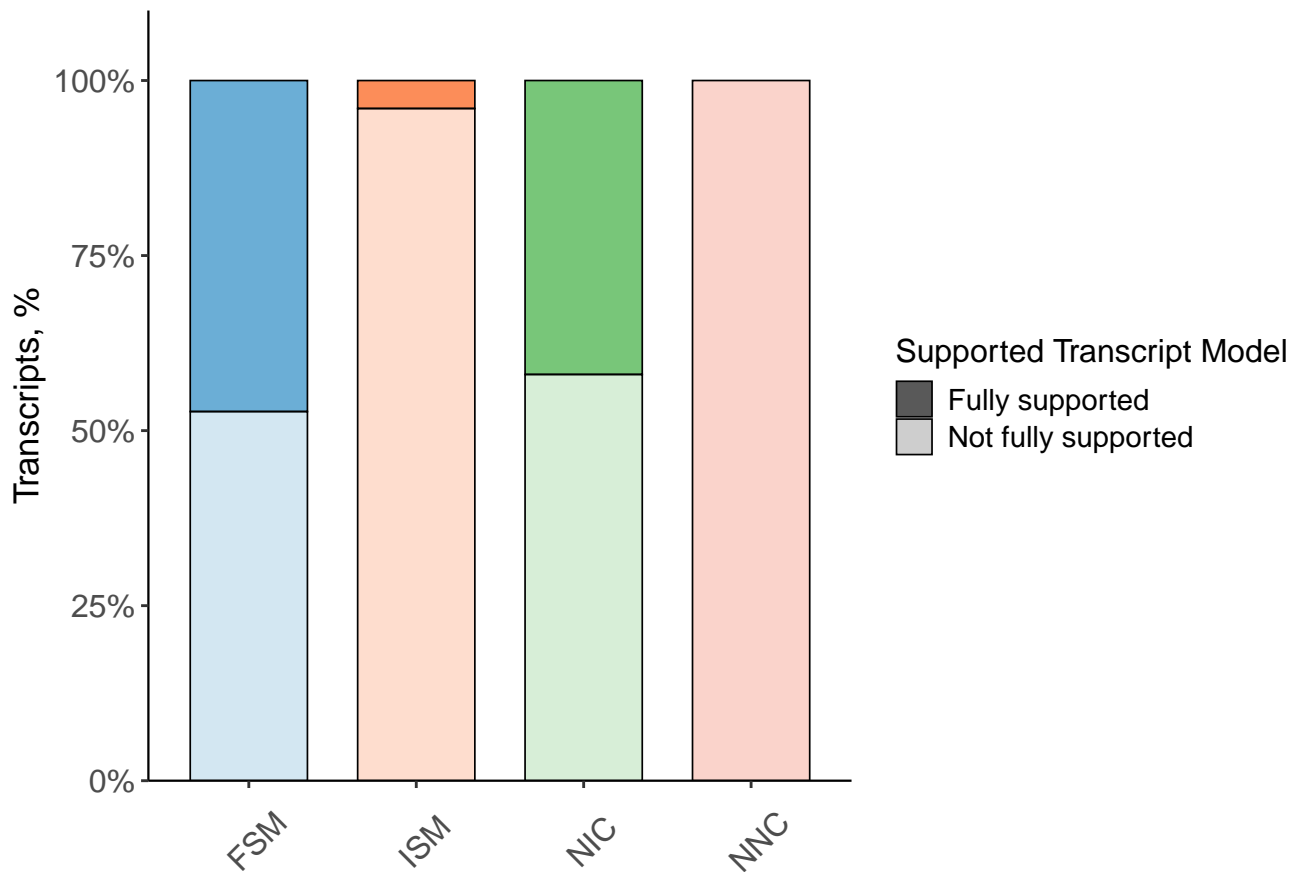
Exon Counts by Subcategory



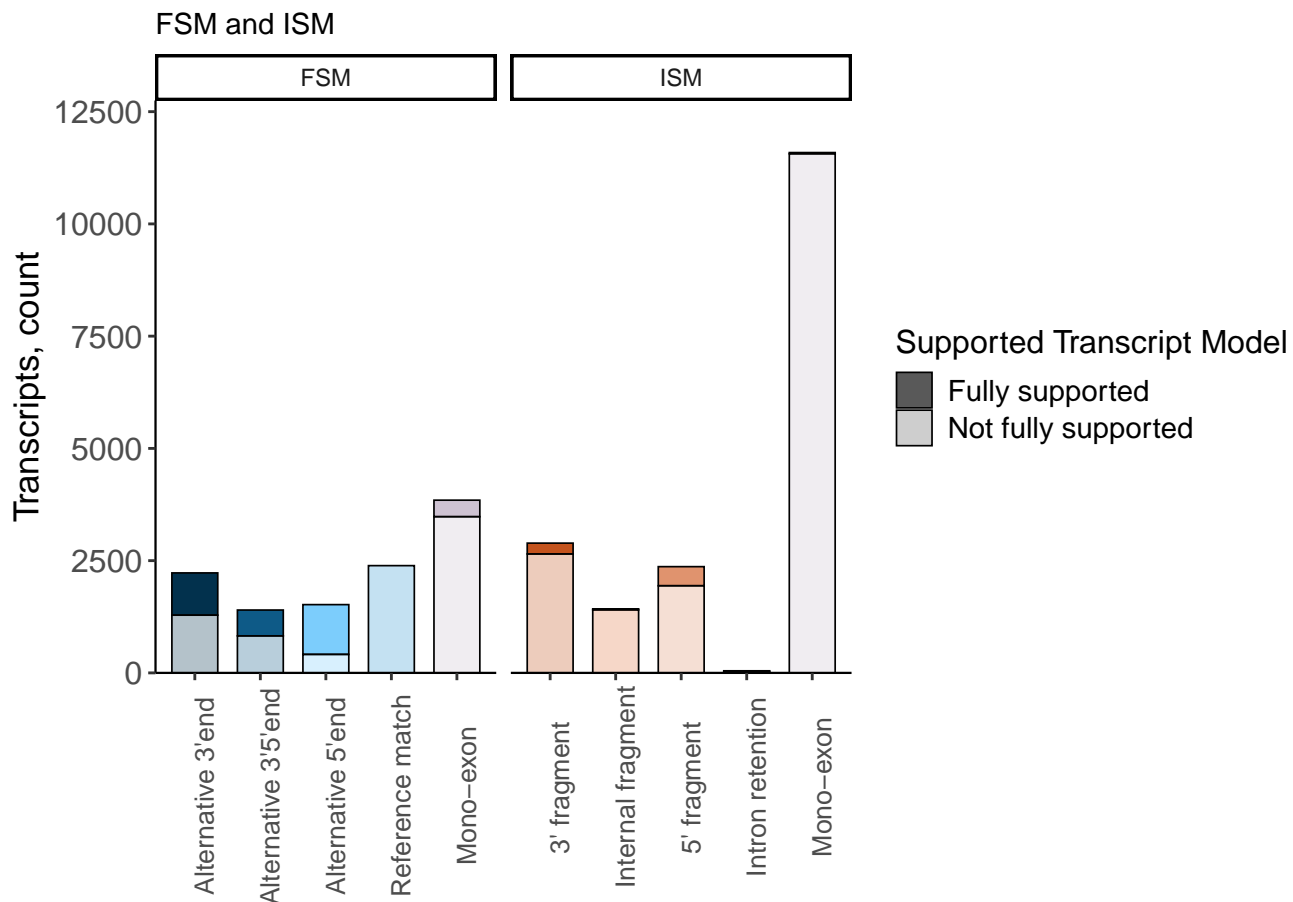
Isoform Distribution Across Structural Categories



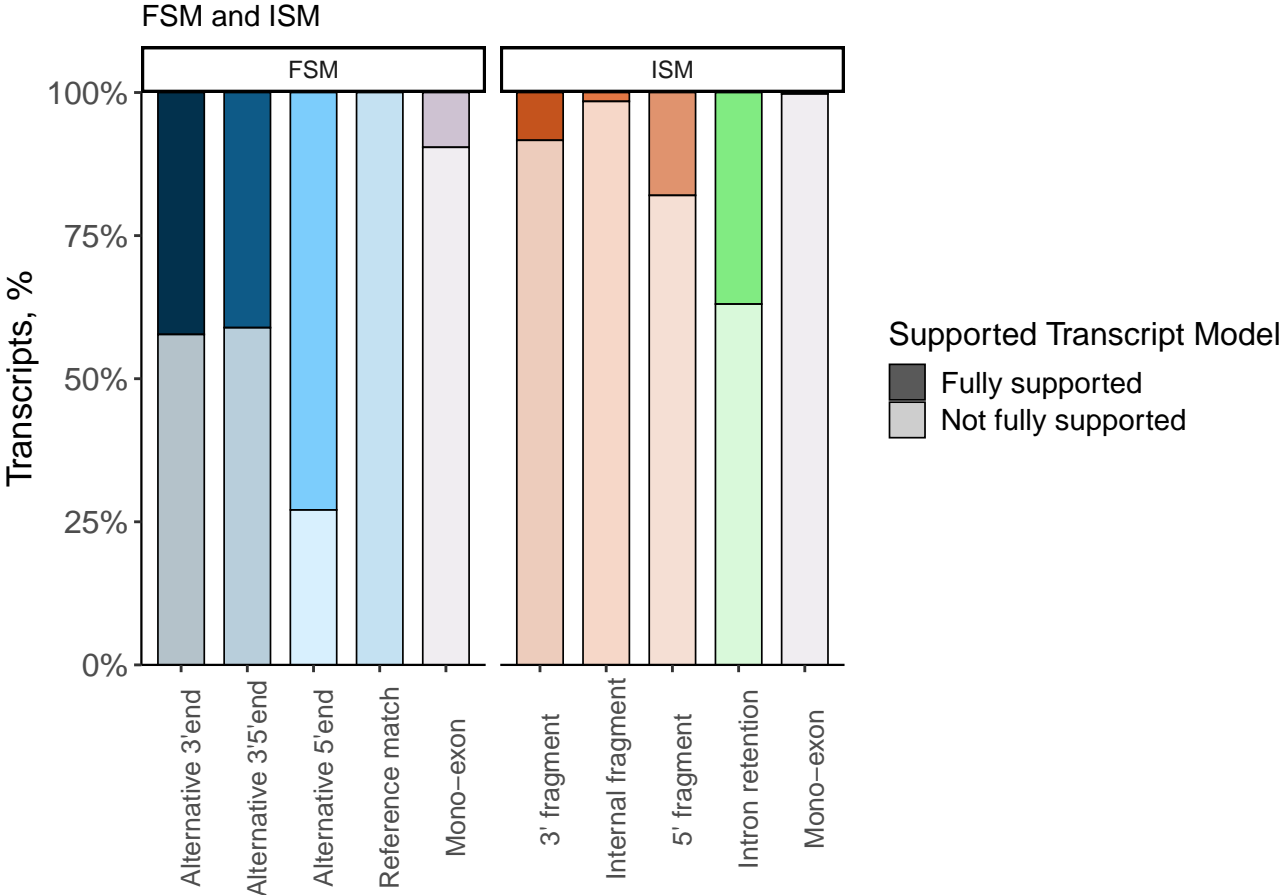
Isoform Distribution Across Structural Categories



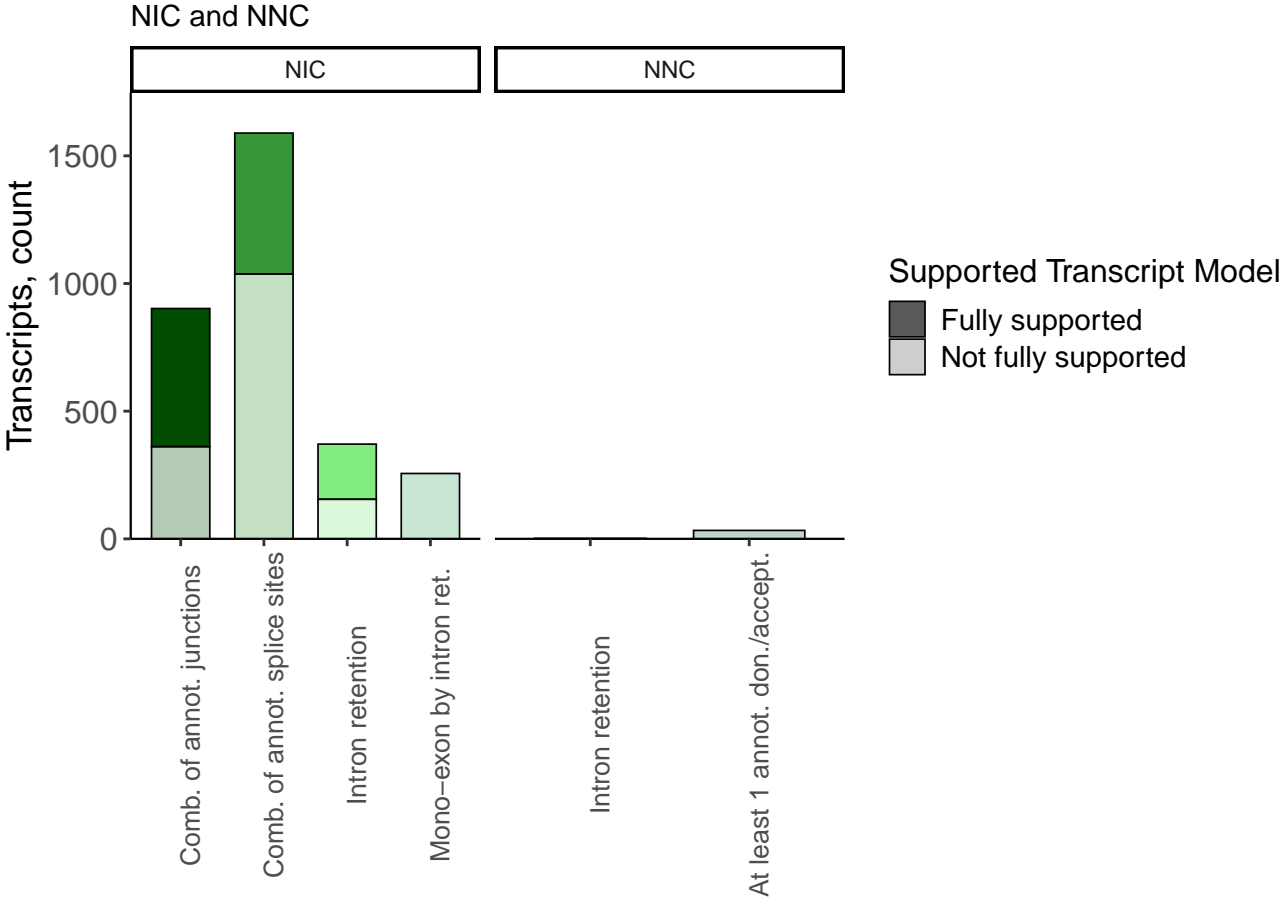
Isoform Distribution Across Structural Subcategories



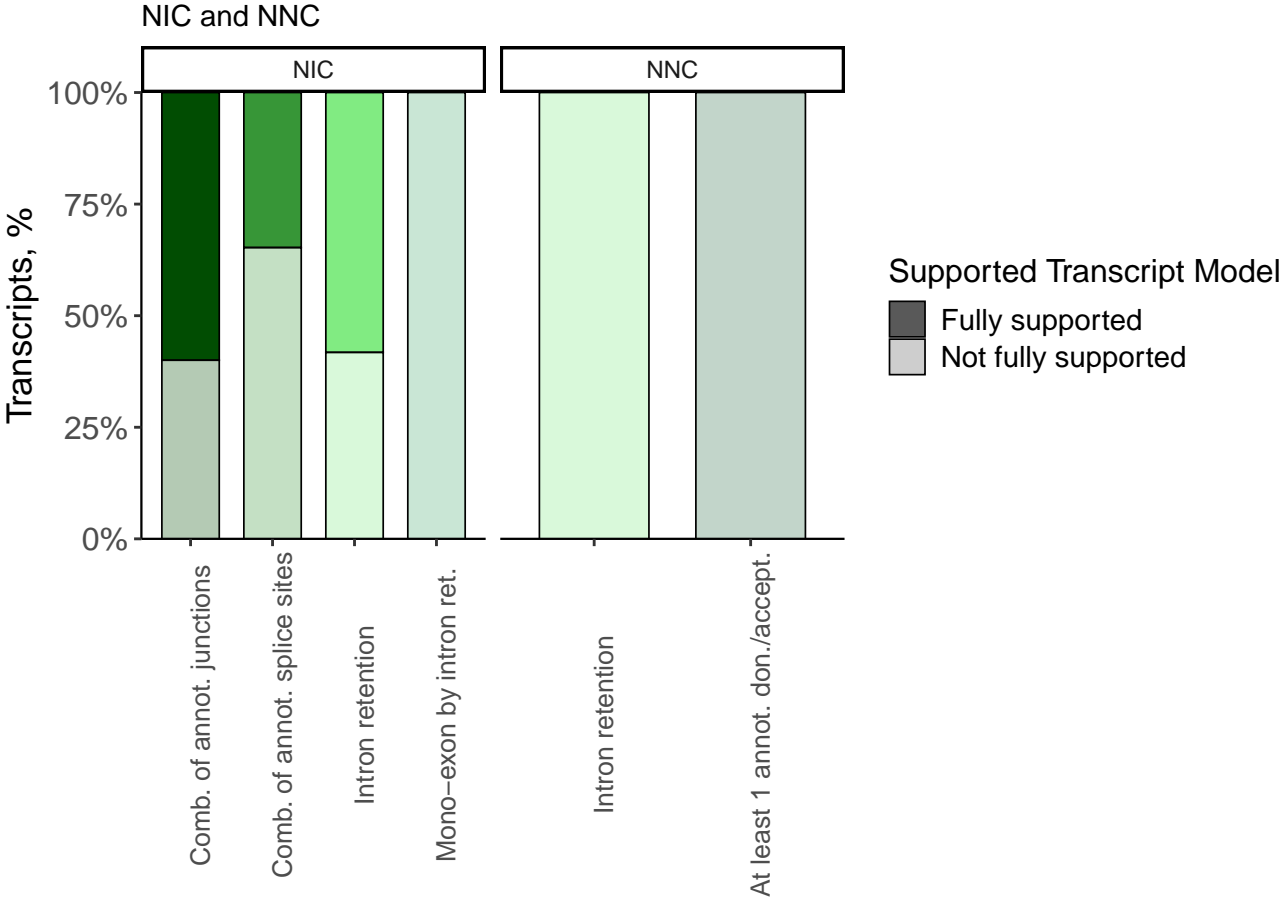
Isoform Distribution Across Structural Subcategories



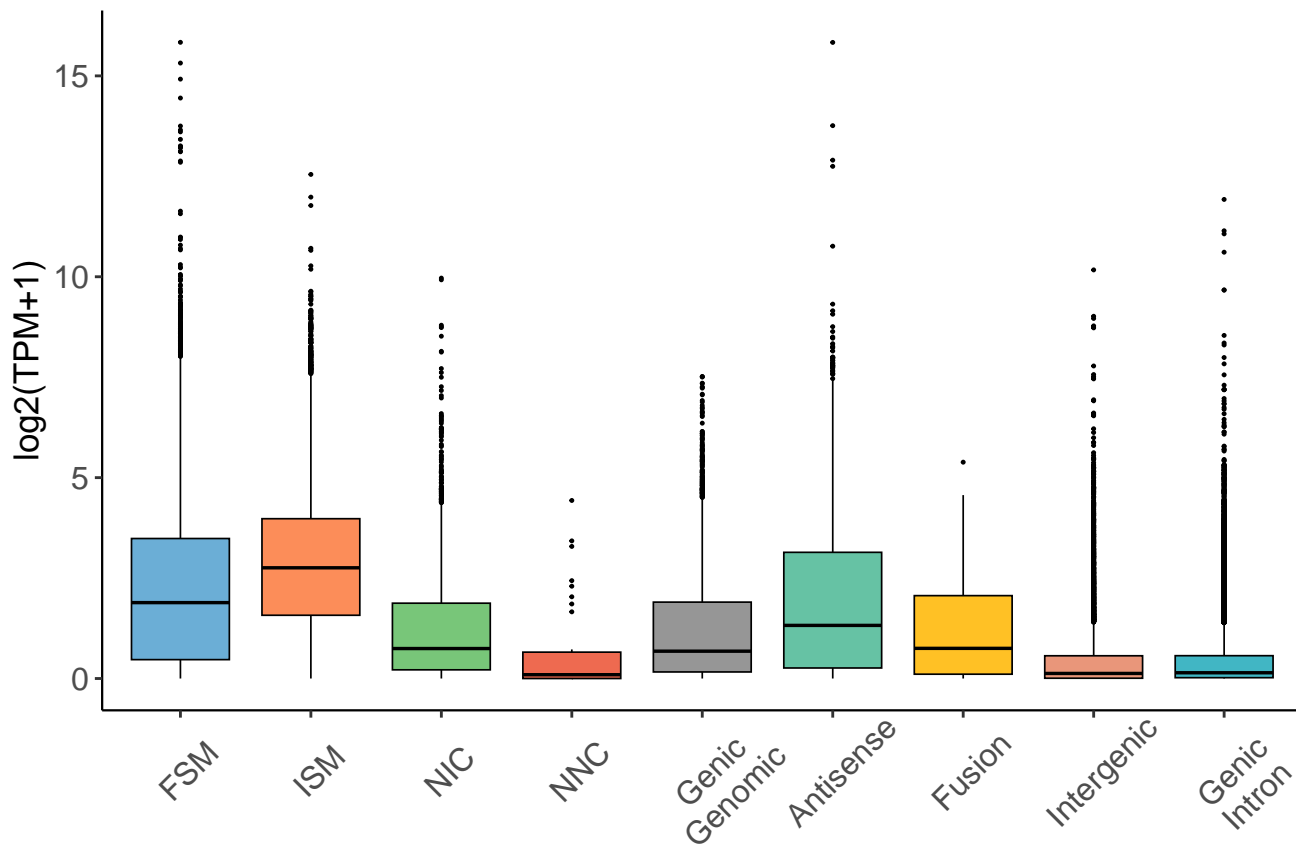
Isoform Distribution Across Structural Subcategories



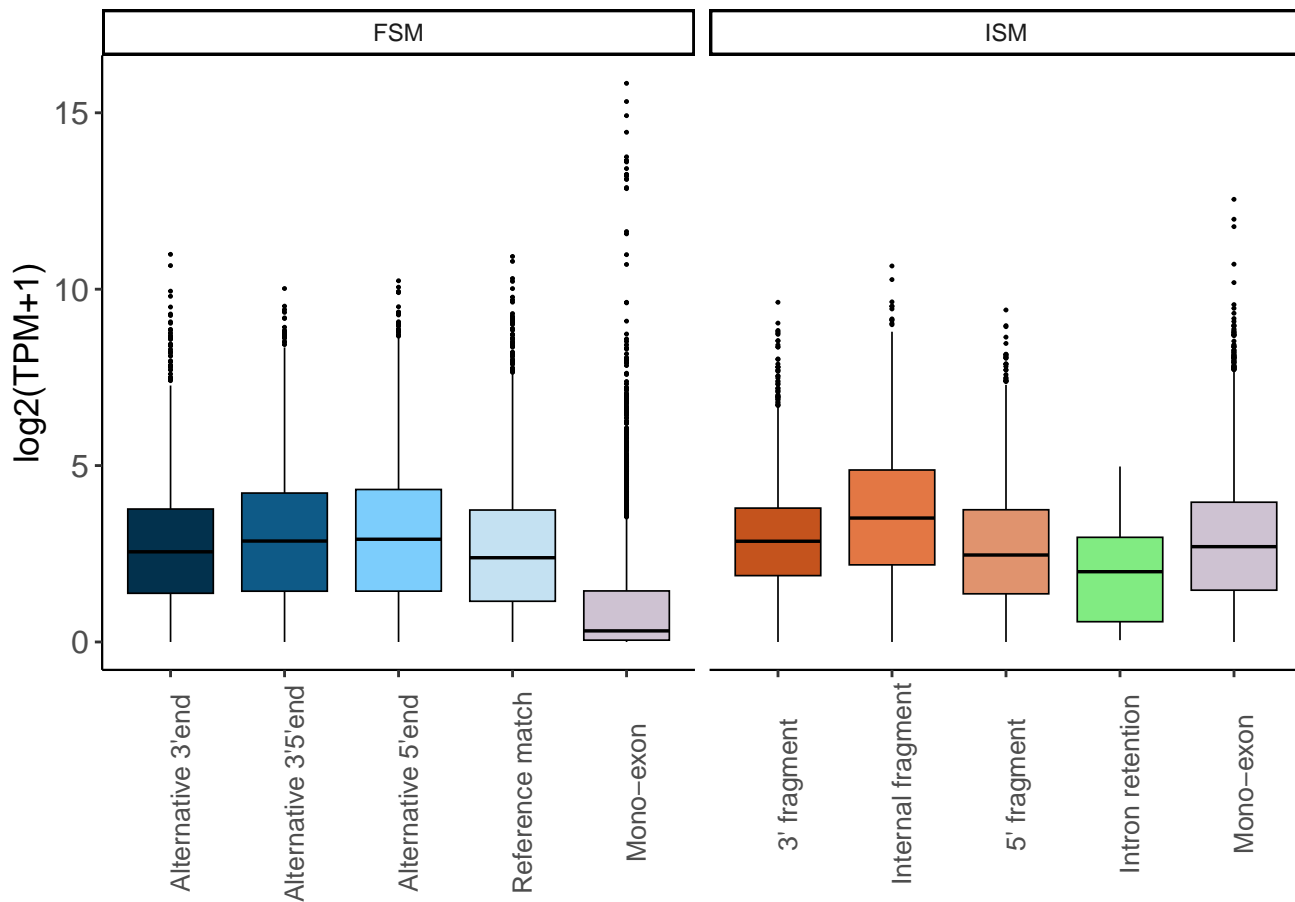
Isoform Distribution Across Structural Subcategories



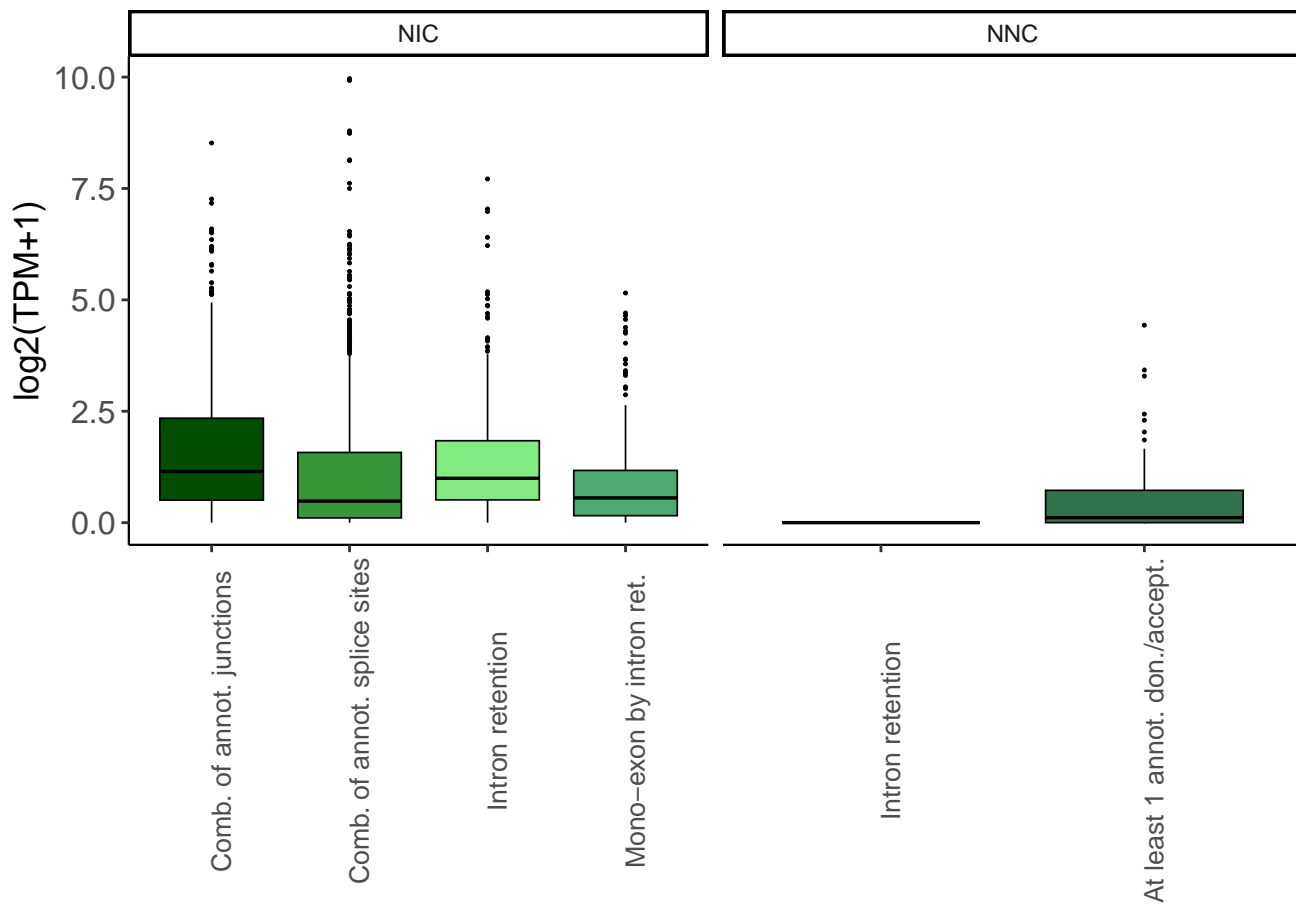
Transcript Expression by Structural Category



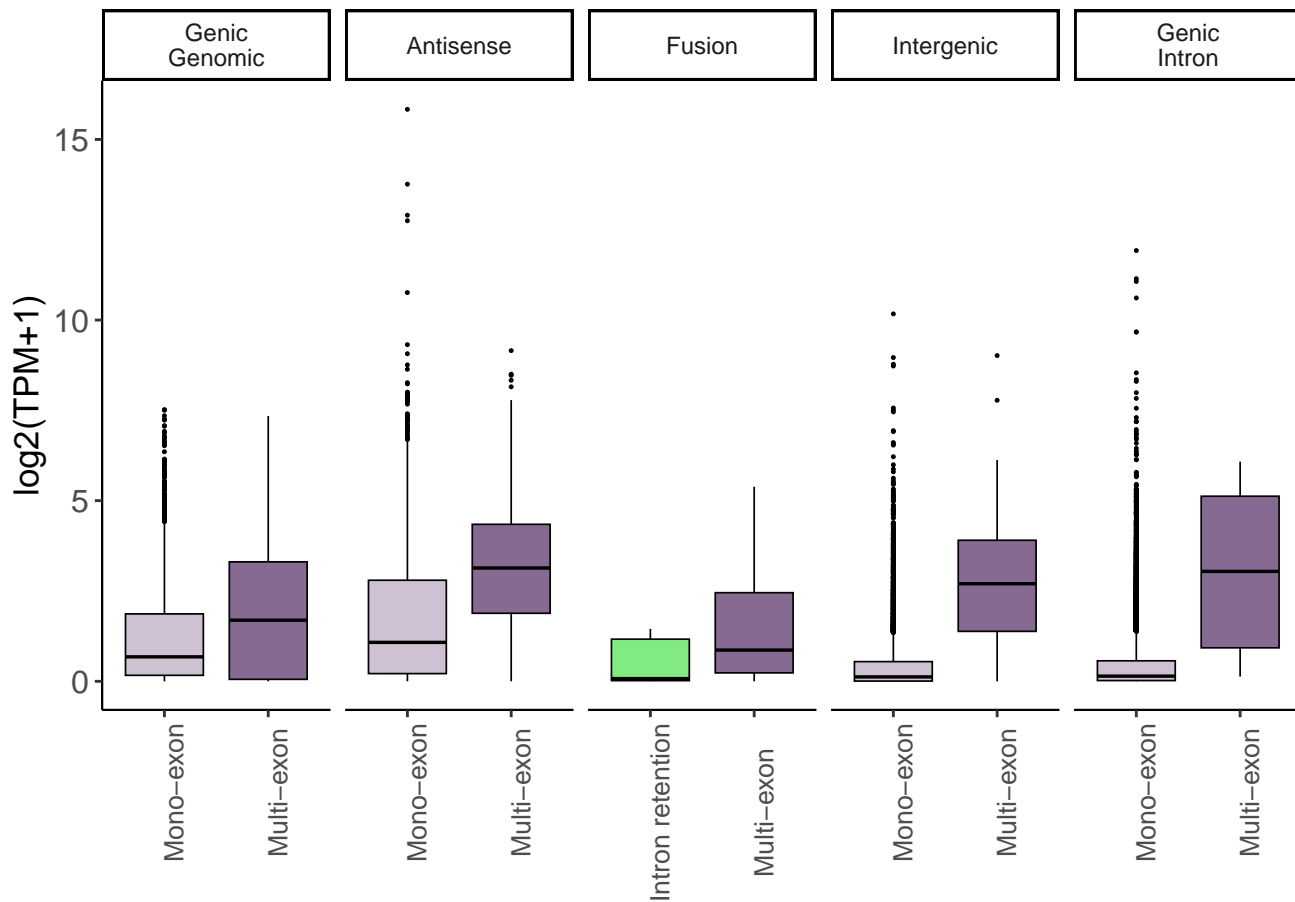
Transcript Expression by Subcategory



Transcript Expression by Subcategory

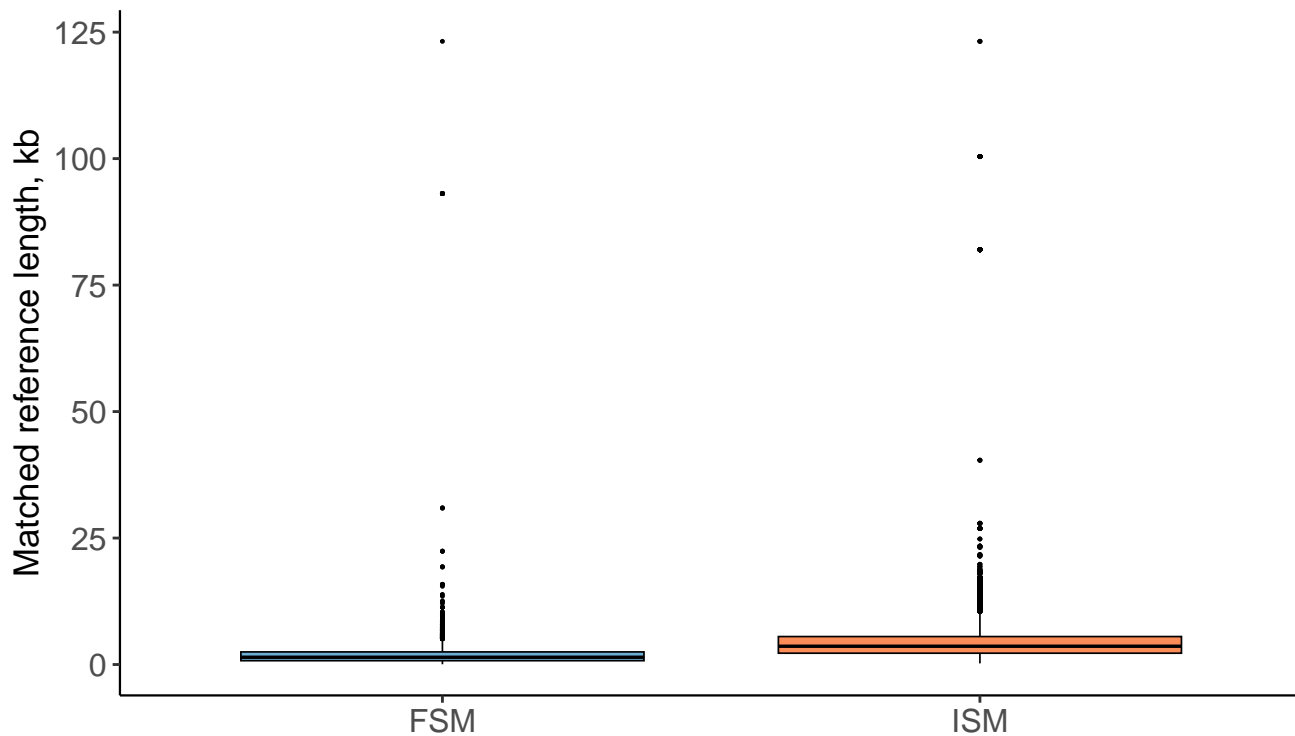


Transcript Expression by Subcategory



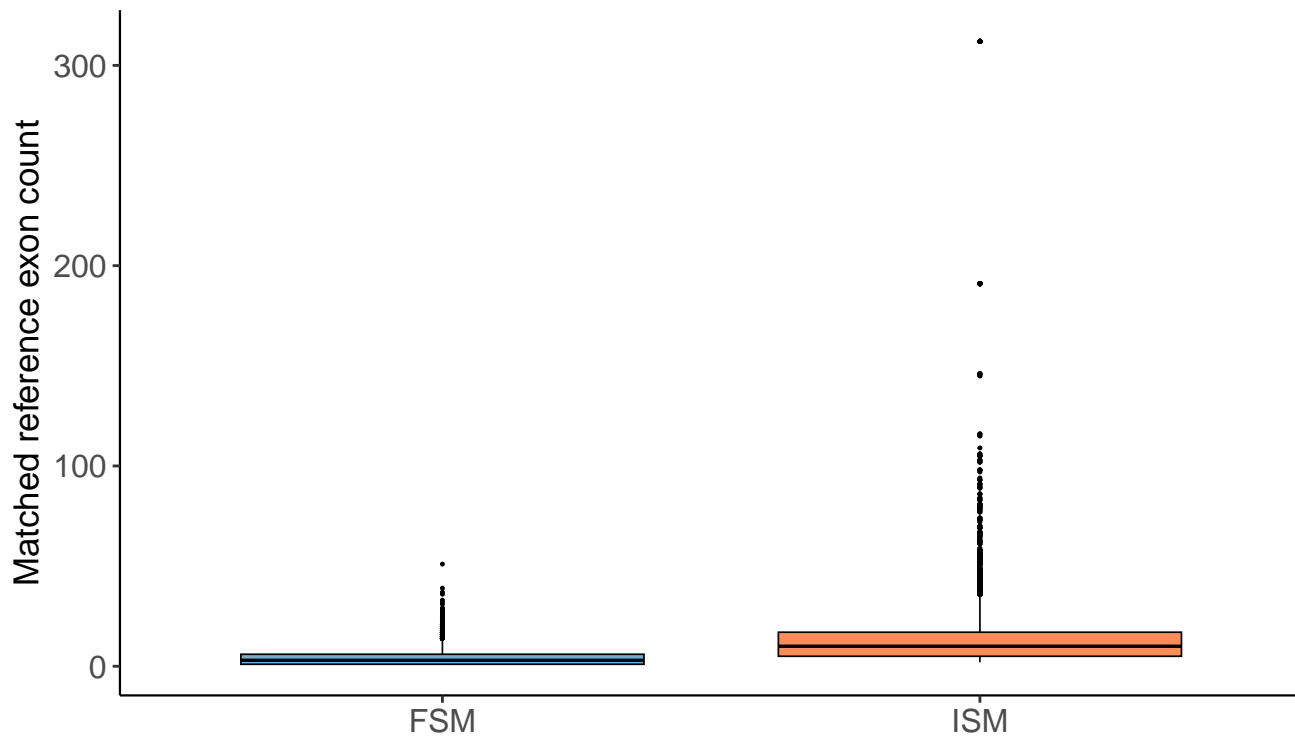
Length Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

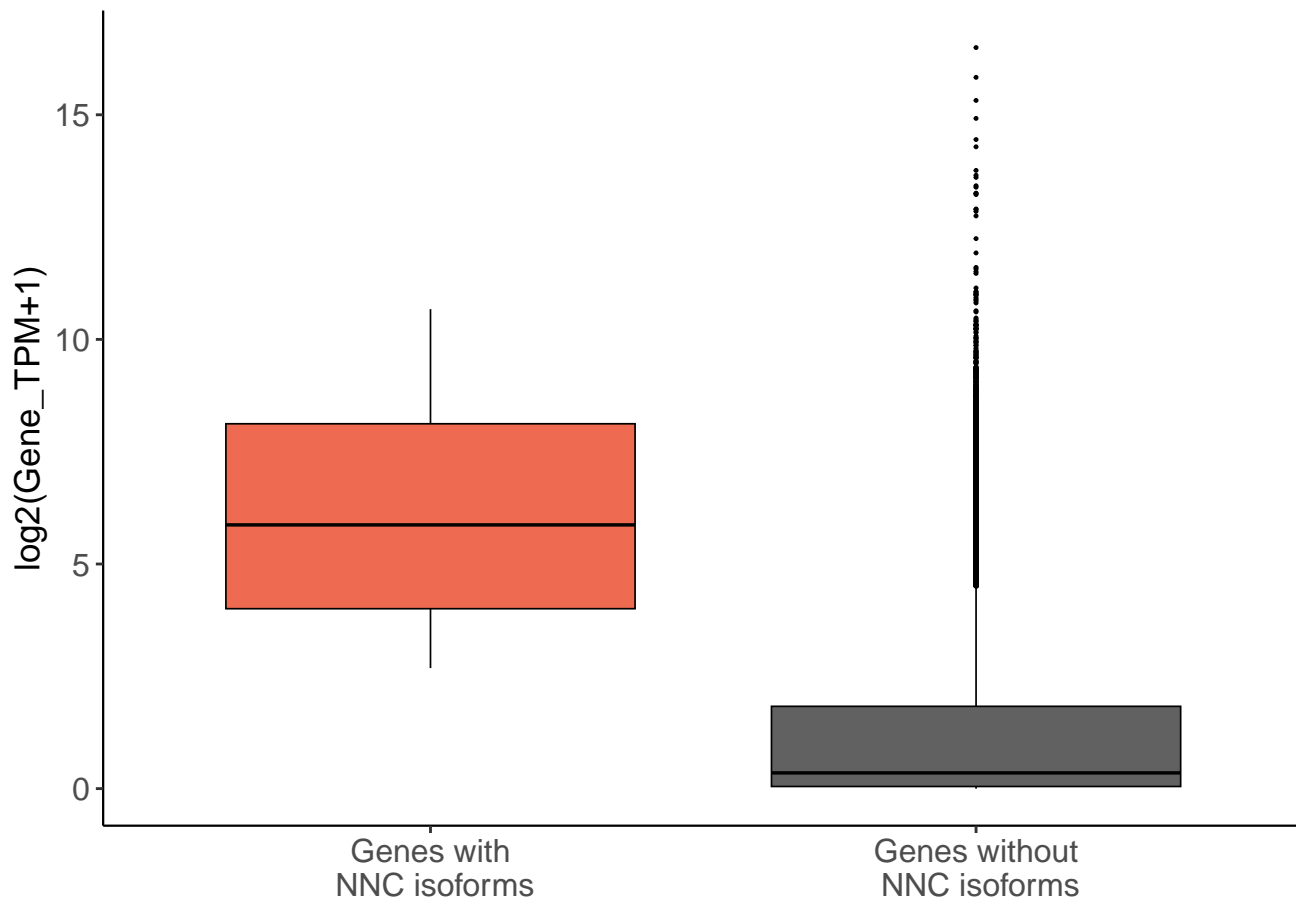


Exon Count Distribution of Matched Reference Transcripts

Applicable Only to FSM and ISM Categories

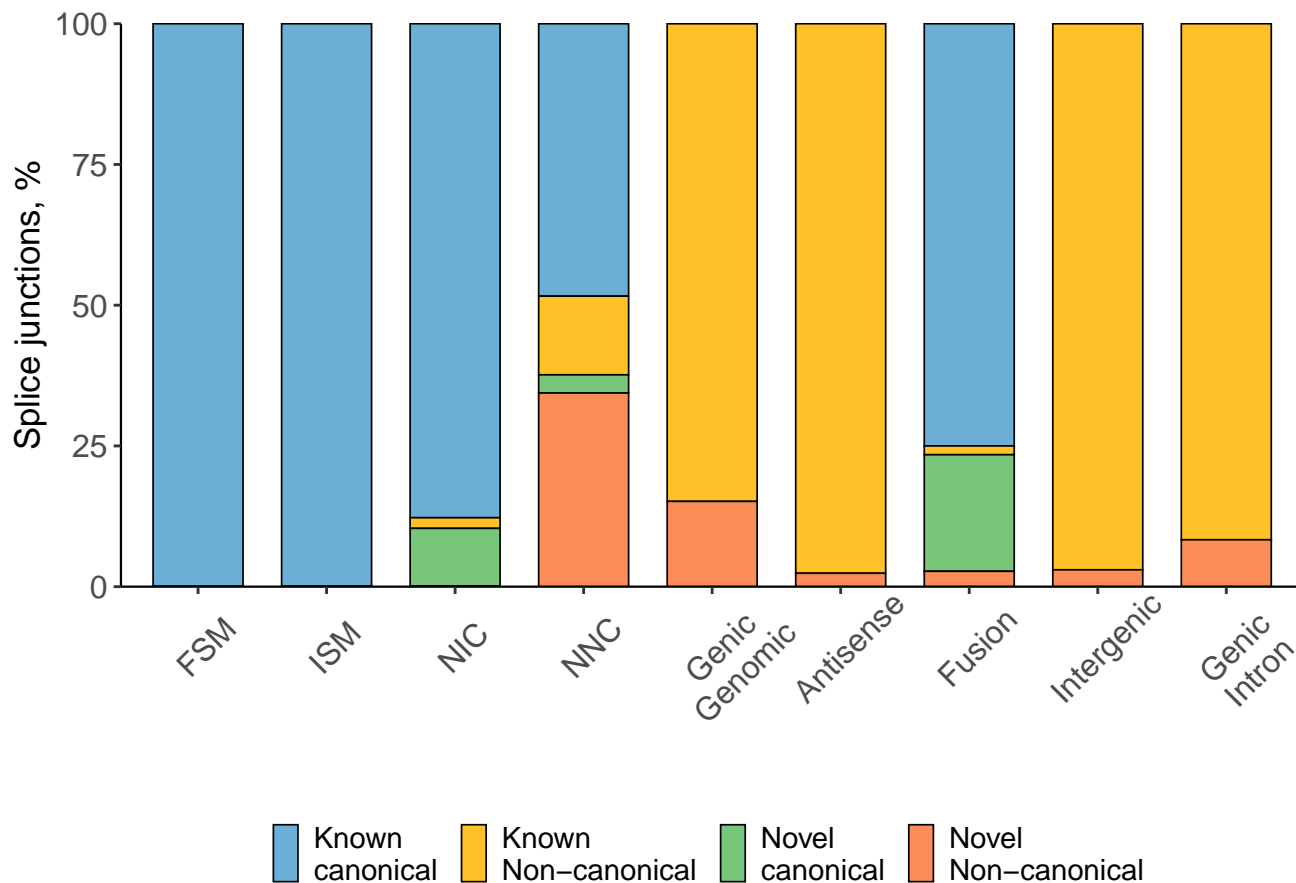


Gene Expression of NNC And Not NNC Containing Genes

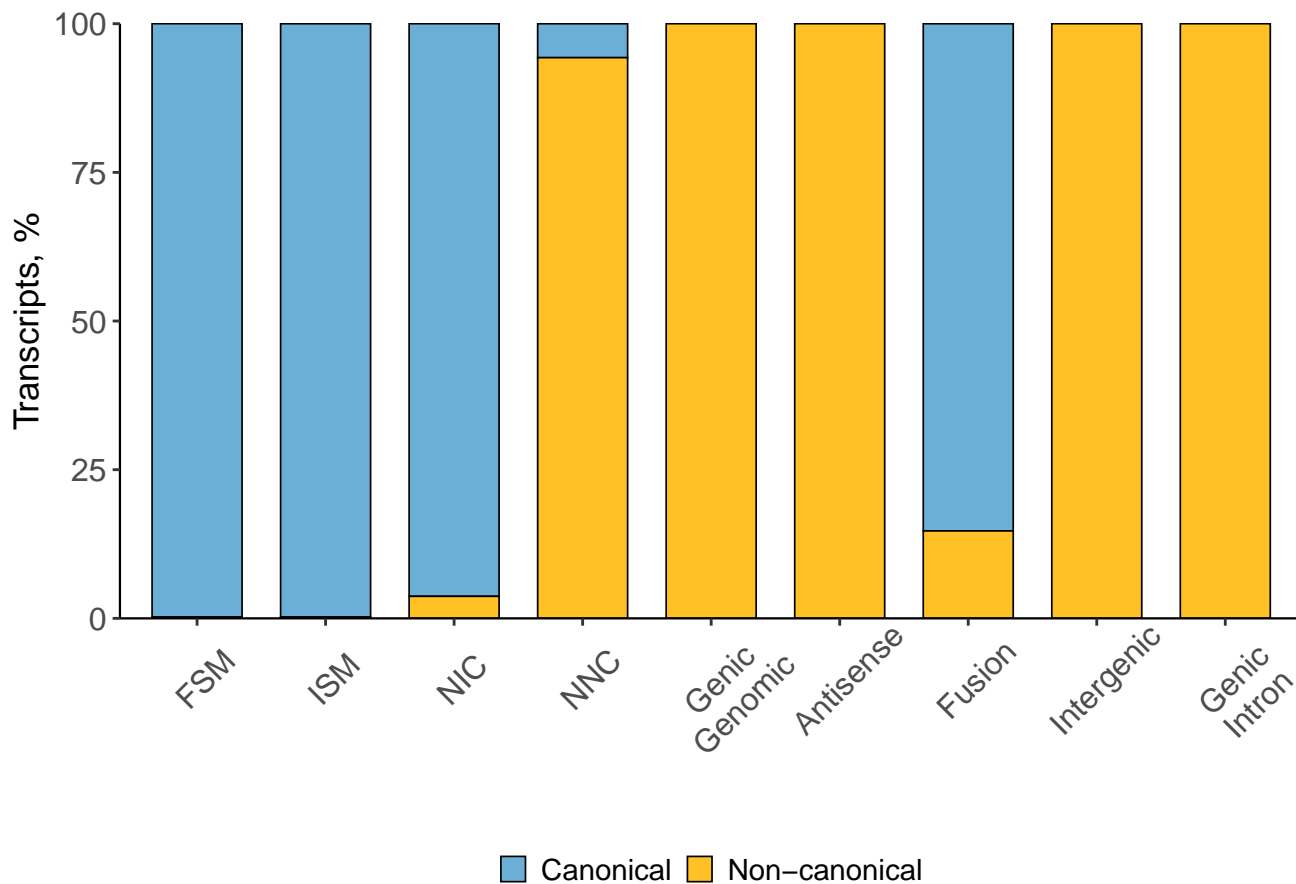


Splice Junction Characterization

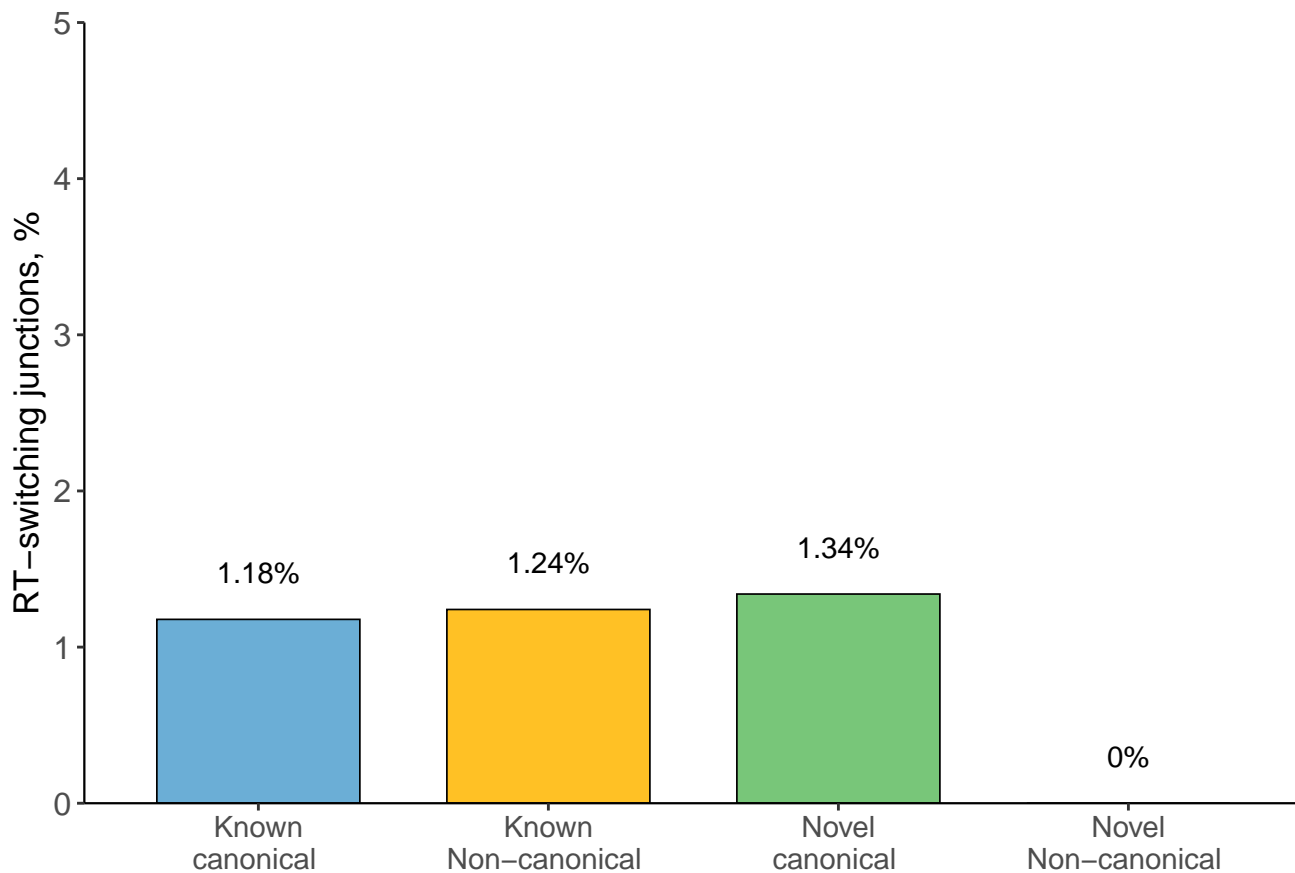
Distribution of Splice Junctions by Structural Classification



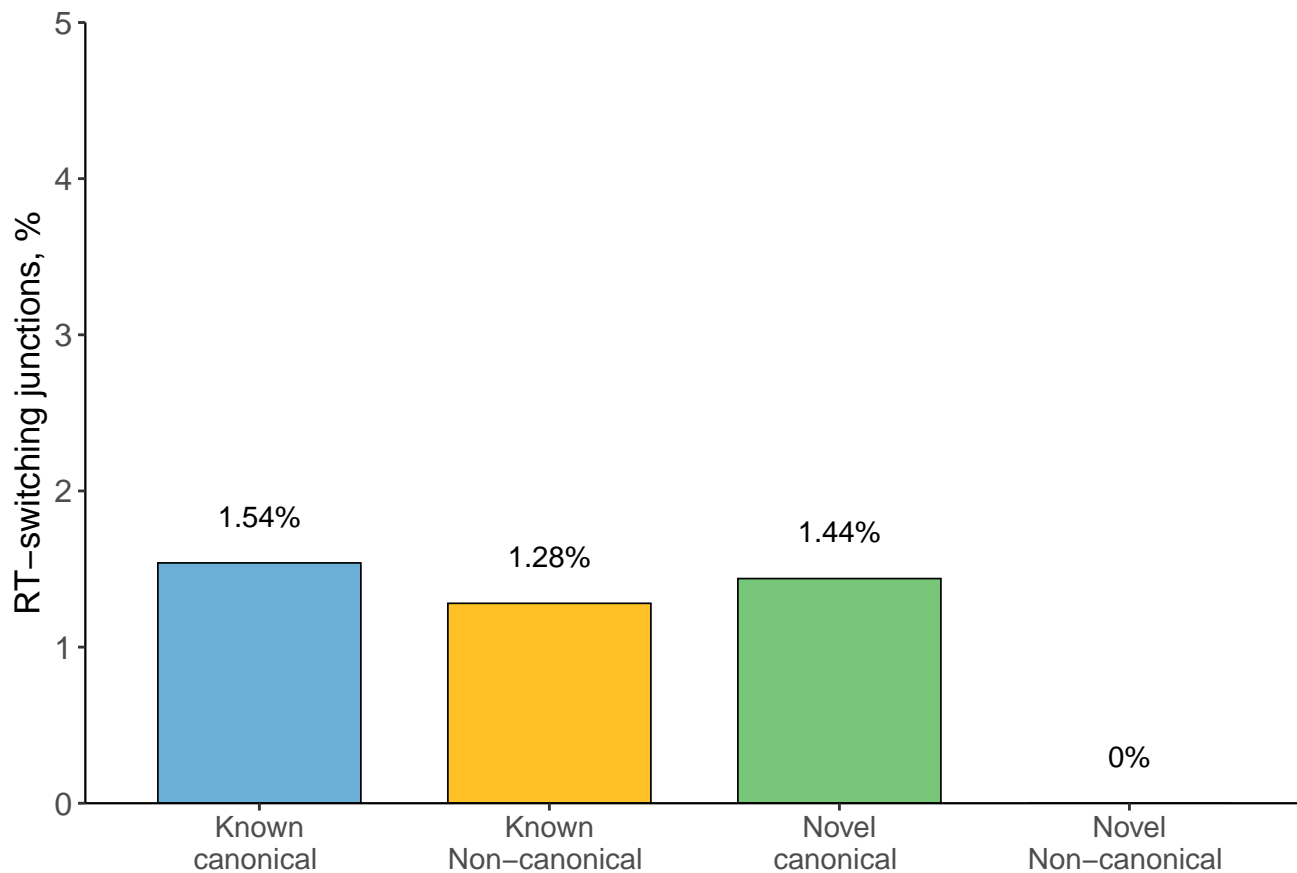
Distribution of Transcripts by Splice Junctions



RT-Switching All Junctions



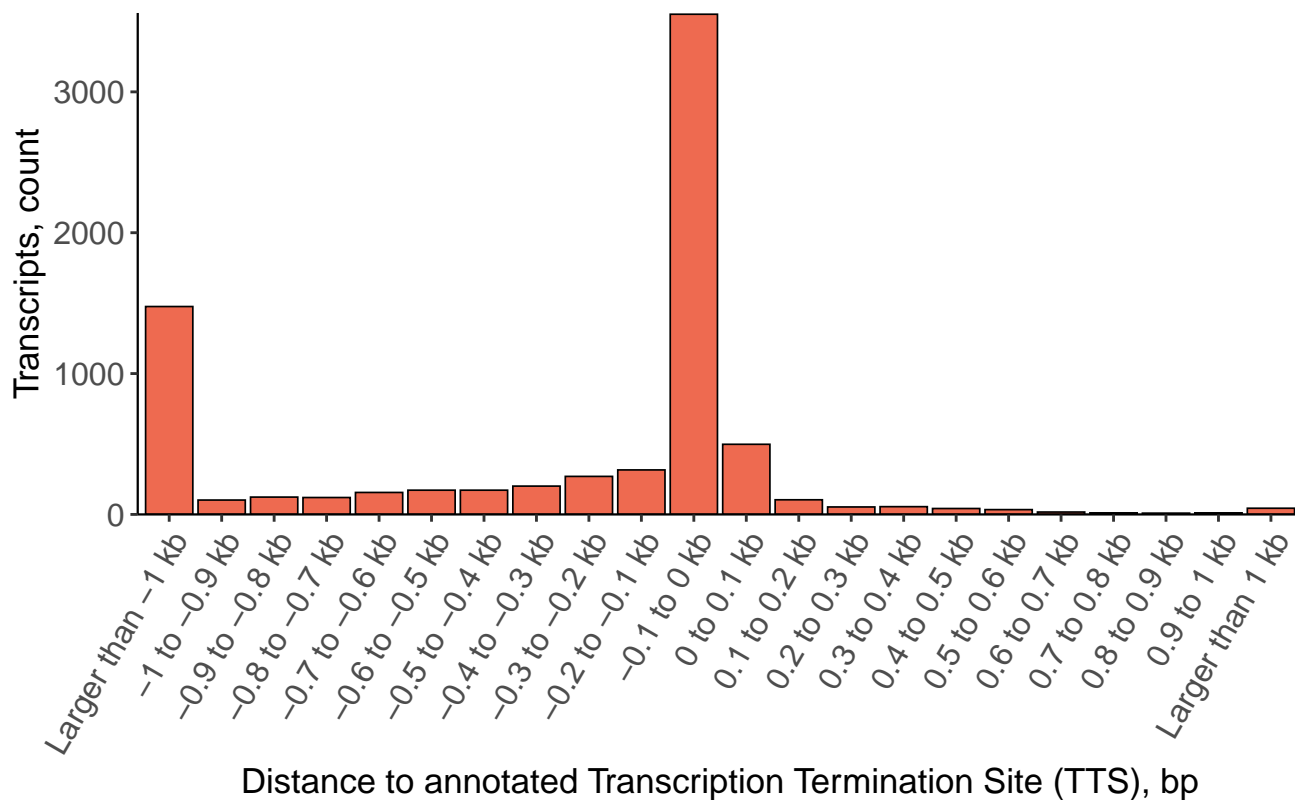
Unique Junctions RT-switching



Comparison With Annotated TSS and TTS

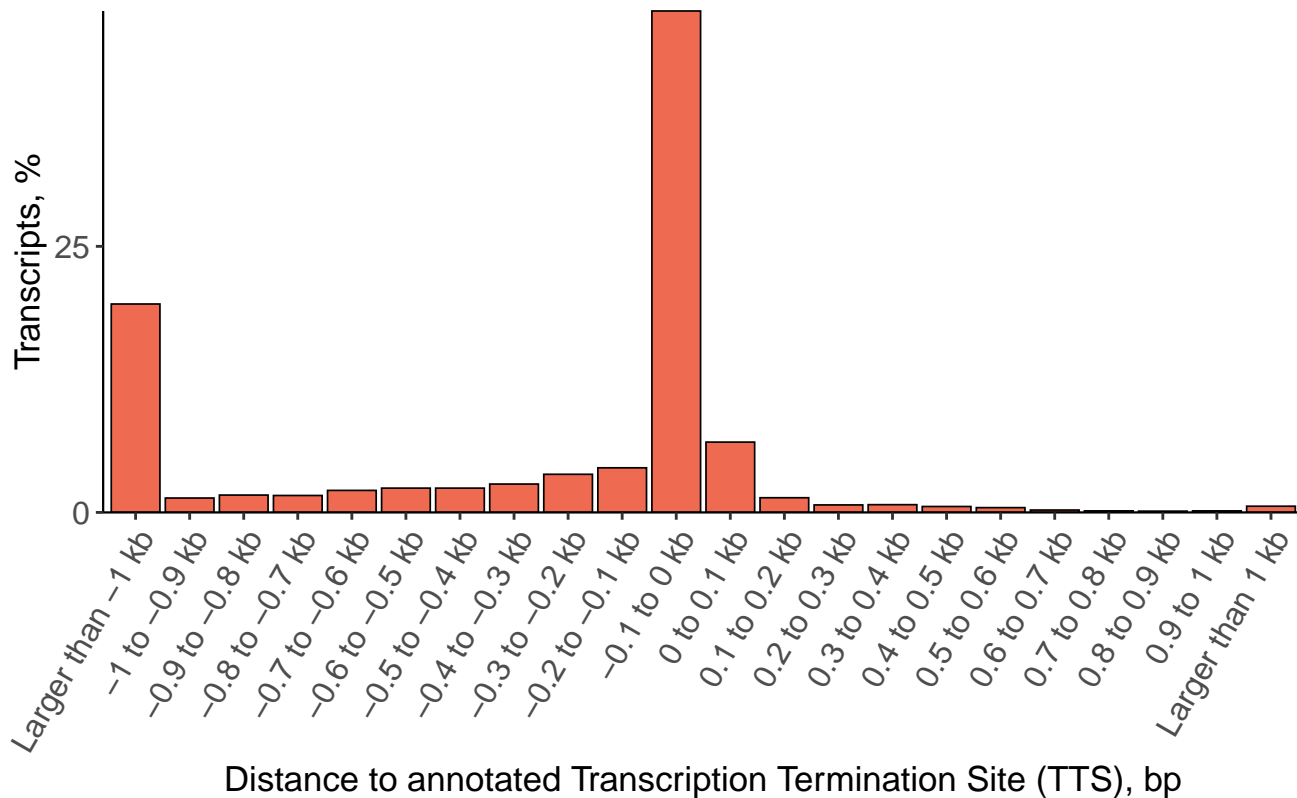
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



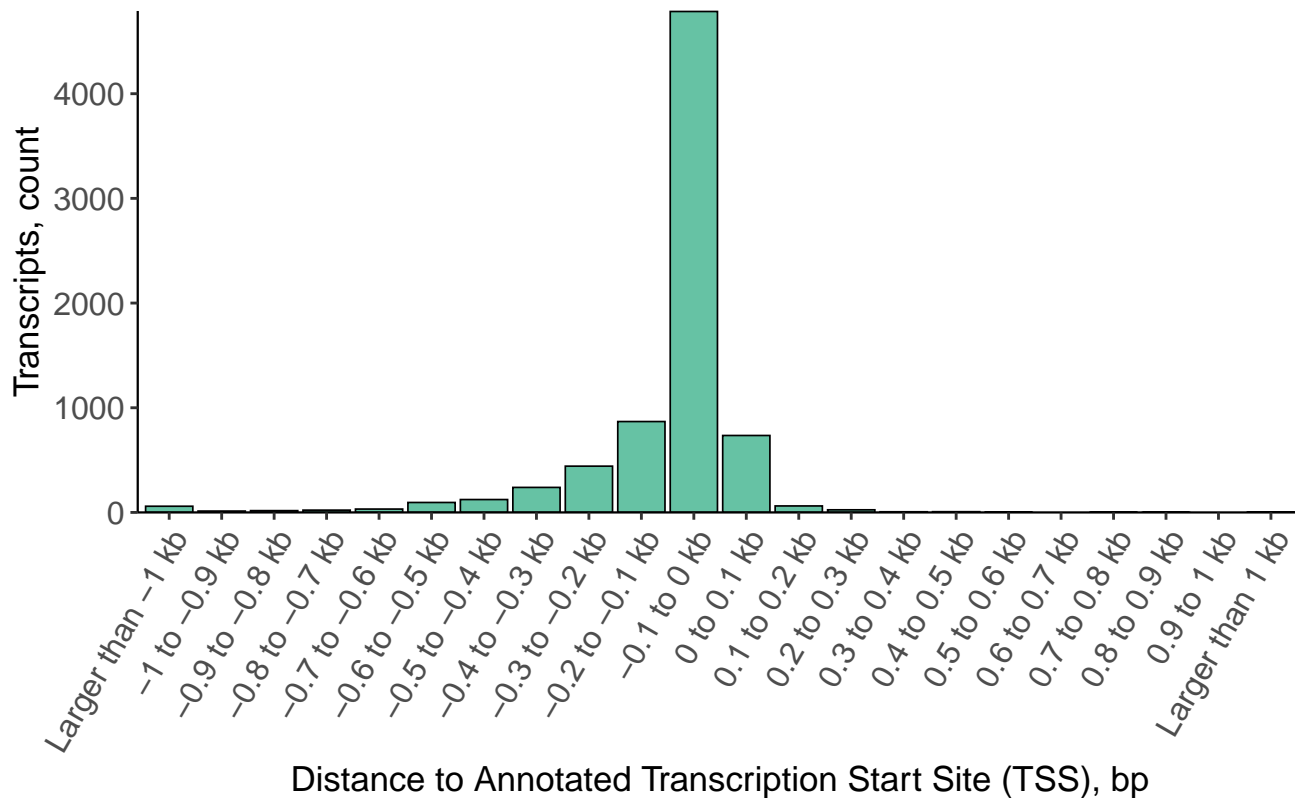
Distance to annotated Transcription Termination Site (TTS) FSM

Negative values indicate upstream of annotated termination site



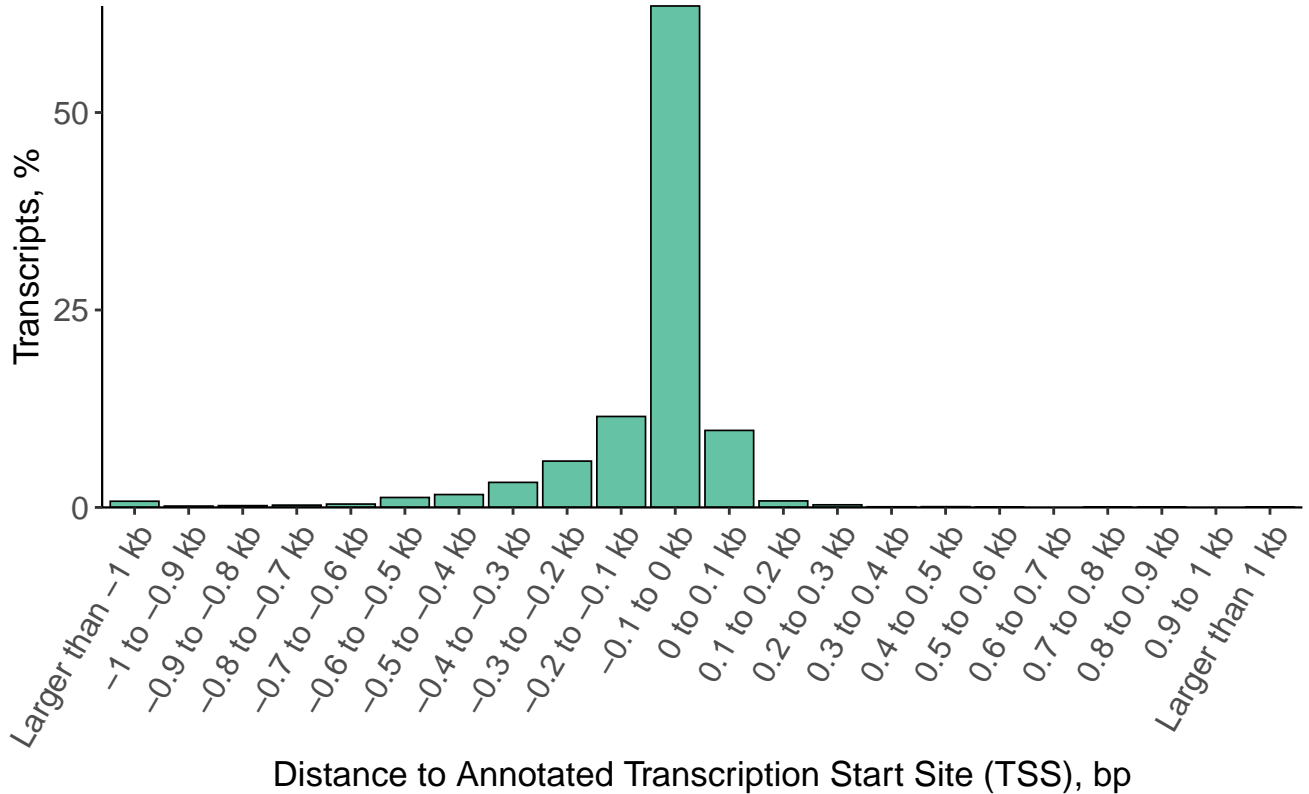
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



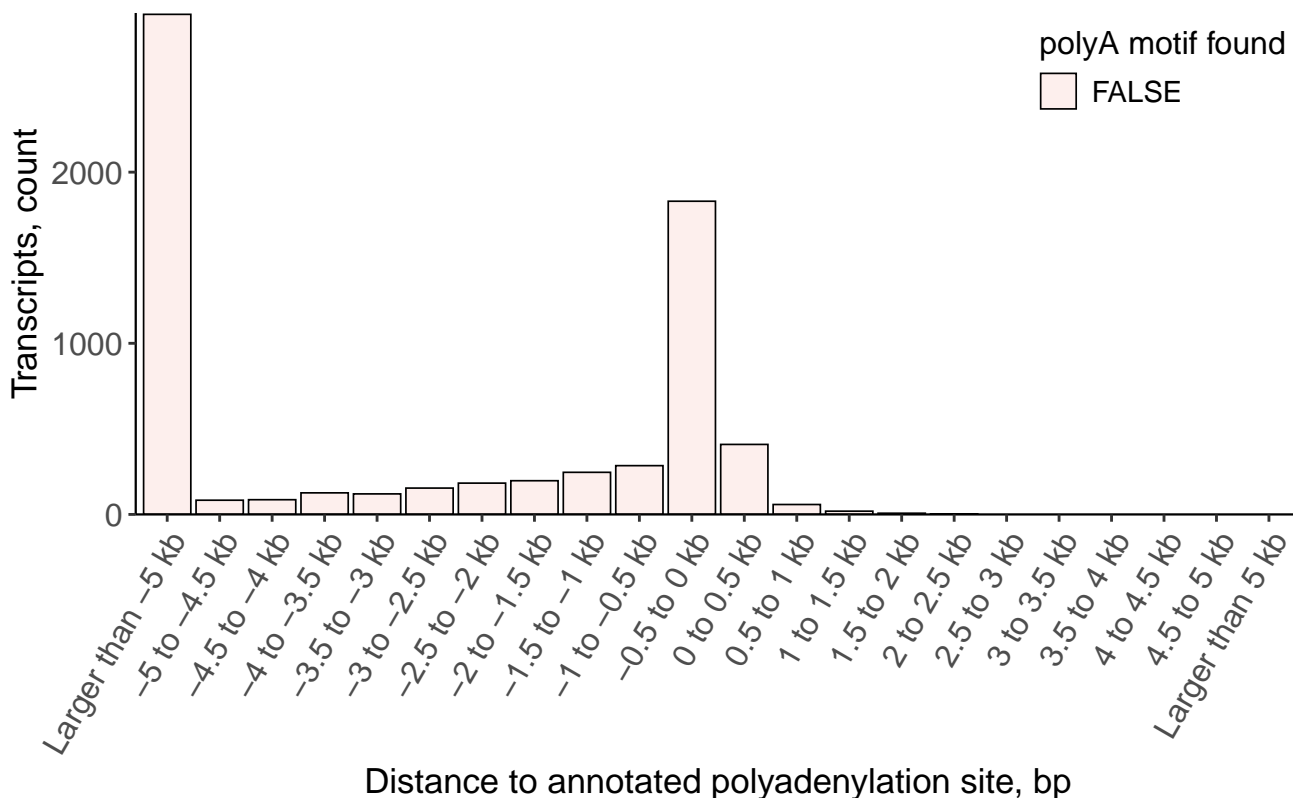
Distance to Annotated Transcription Start Site for FSM

Negative values indicate downstream of annotated TSS



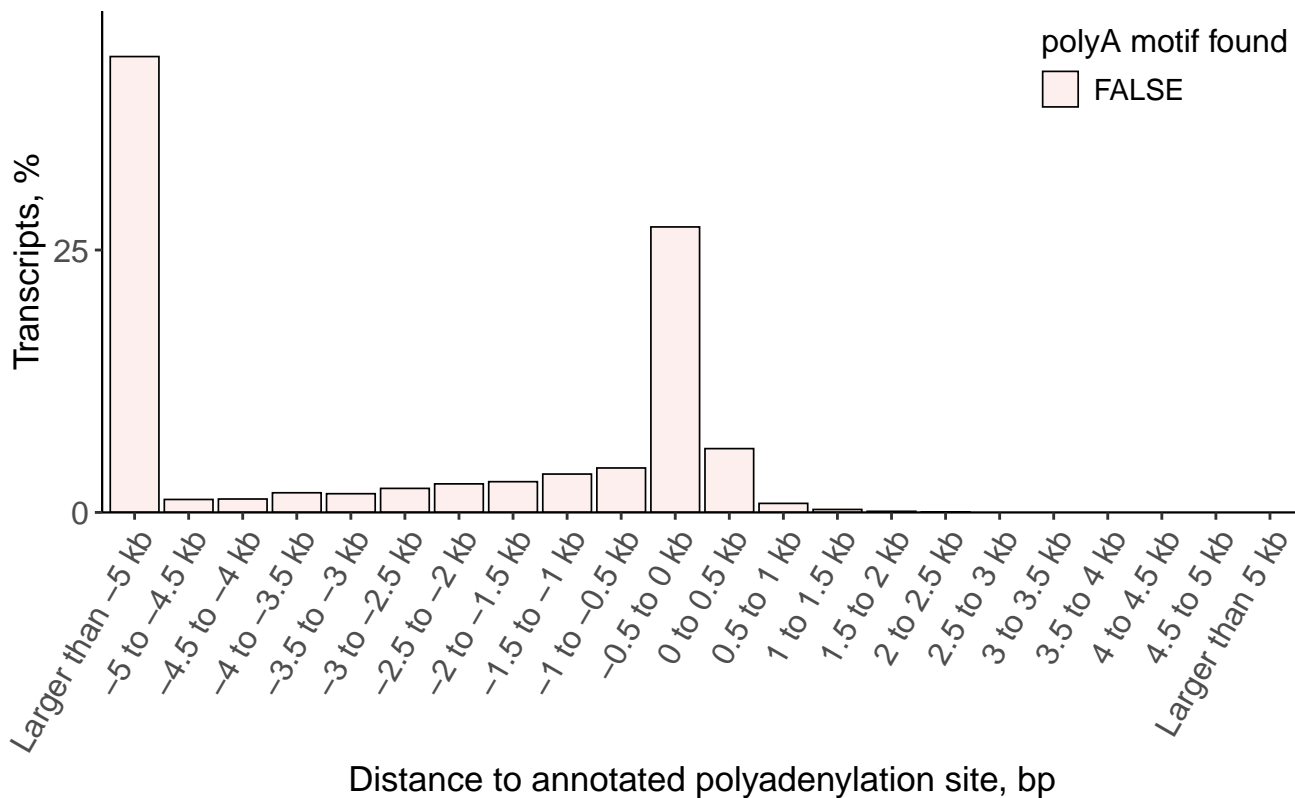
Distance to Annotated Transcription Termination Site (TTS)

Negative values indicate upstream of annotated TTS



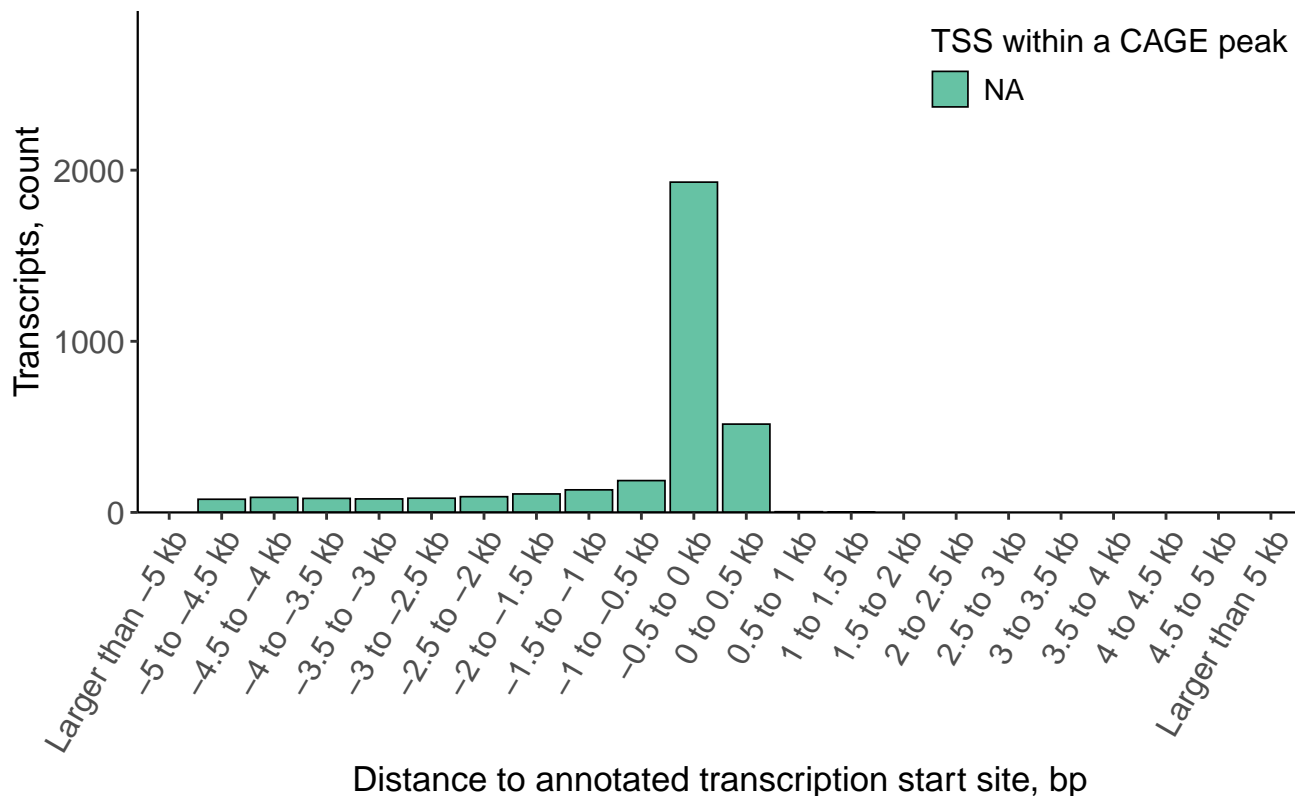
Distance to Annotated Transcription Termination Site (TTS)

Negative values indicate upstream of annotated TTS



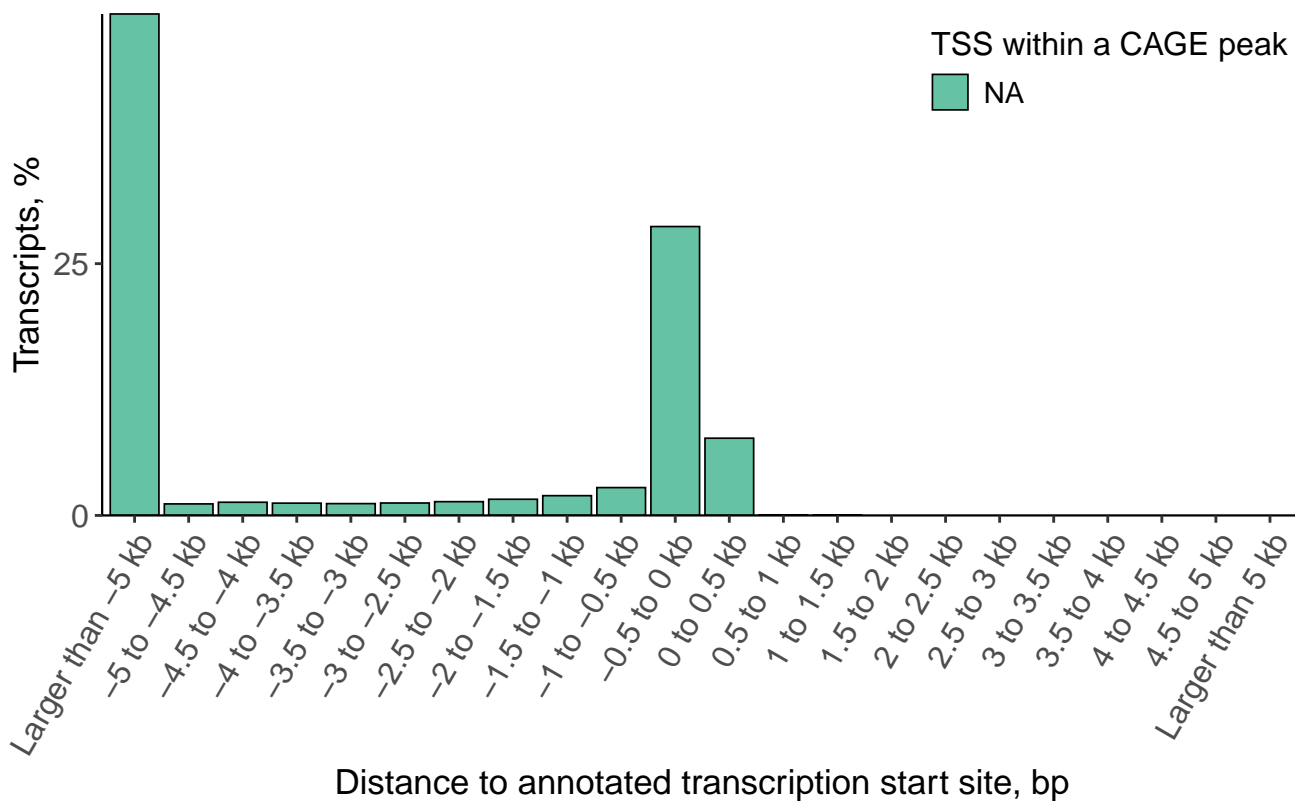
Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS



Distance to Annotated Transcription Start Site for ISM

Negative values indicate downstream of annotated TSS

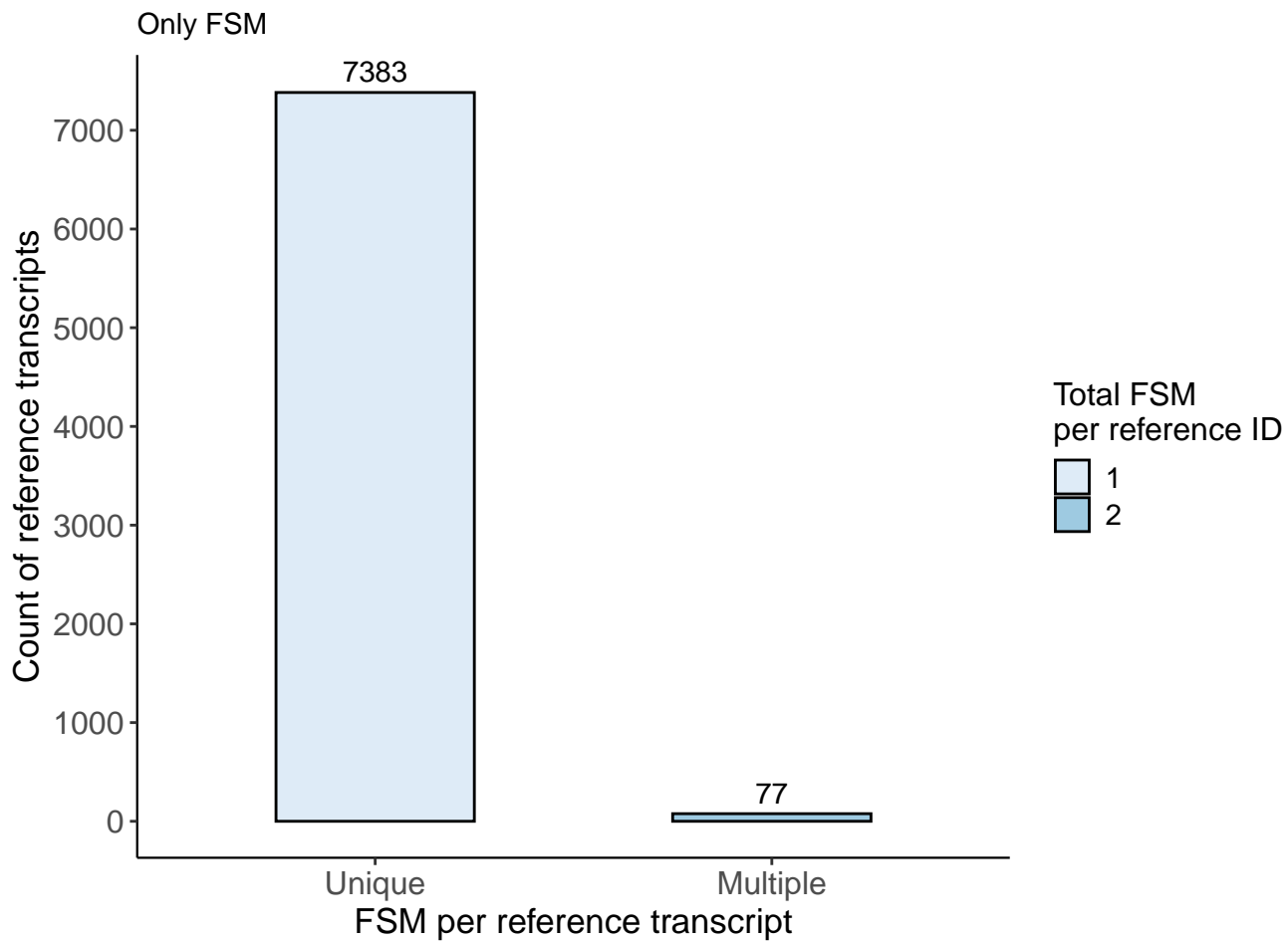


*Comparison With Annotated TSS and TTS
by Subcategories*

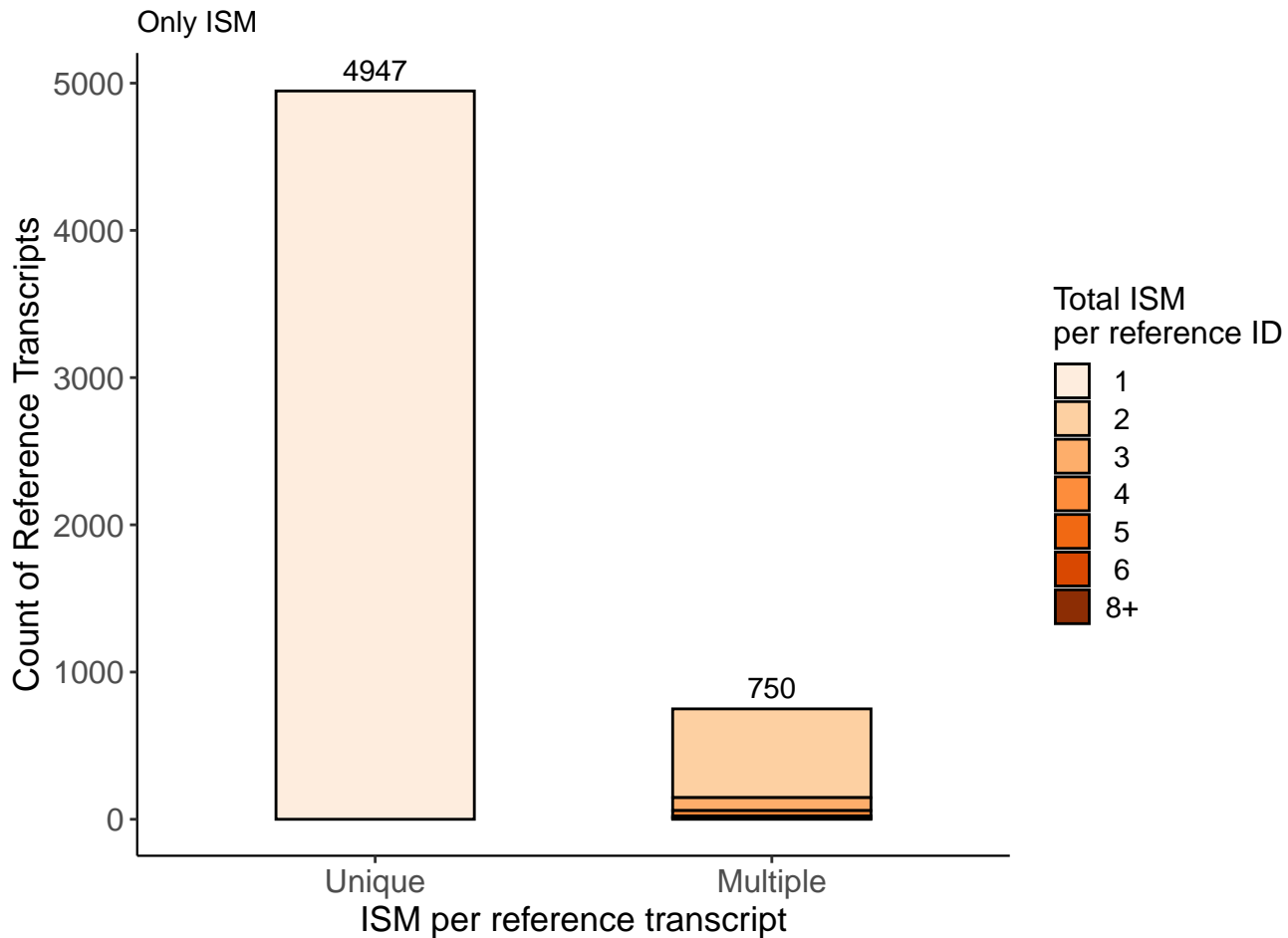
PolyA Distance Analysis

Redundancy Analysis

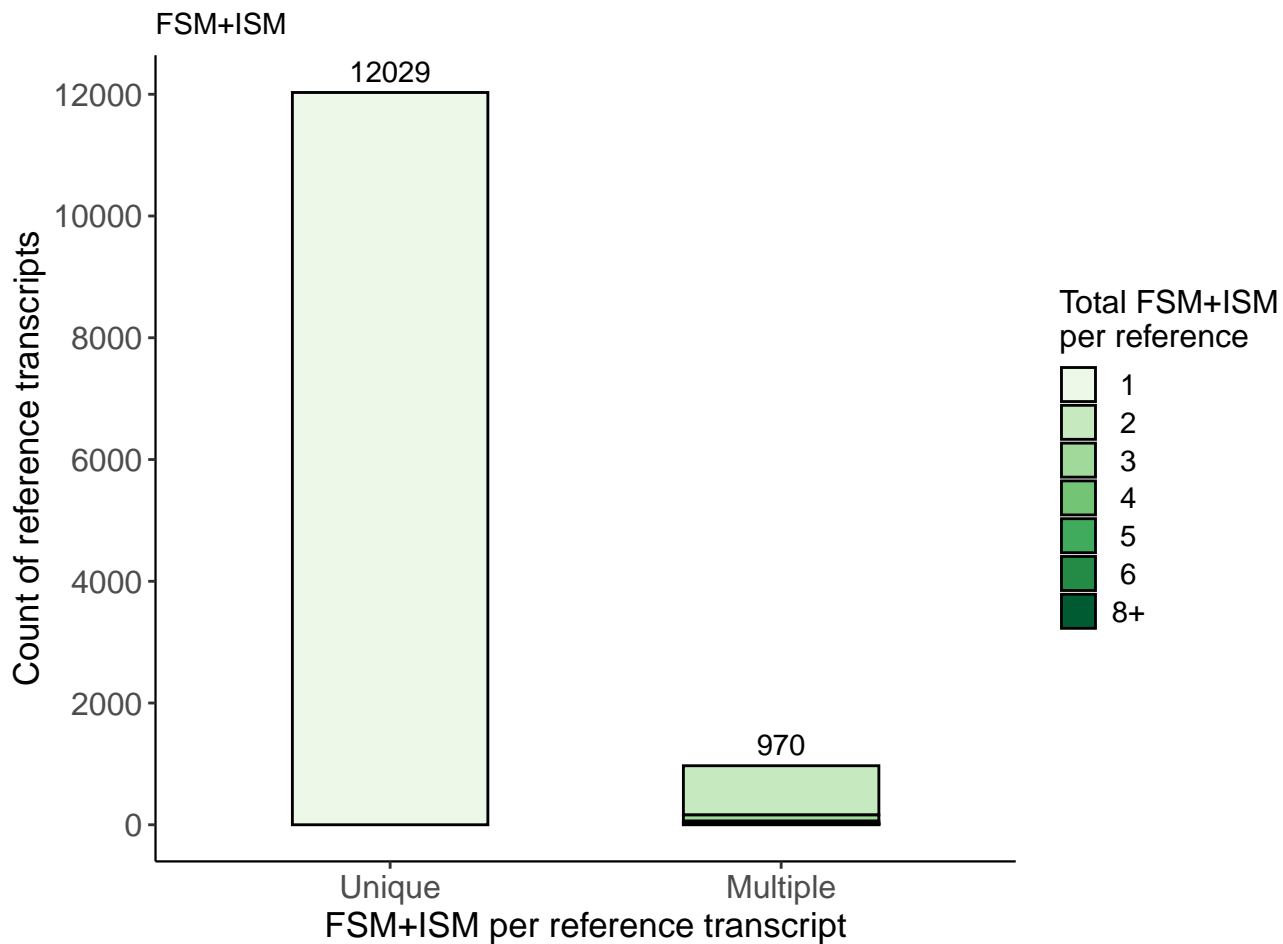
Reference Transcript Redundancy



Reference Transcript Redundancy



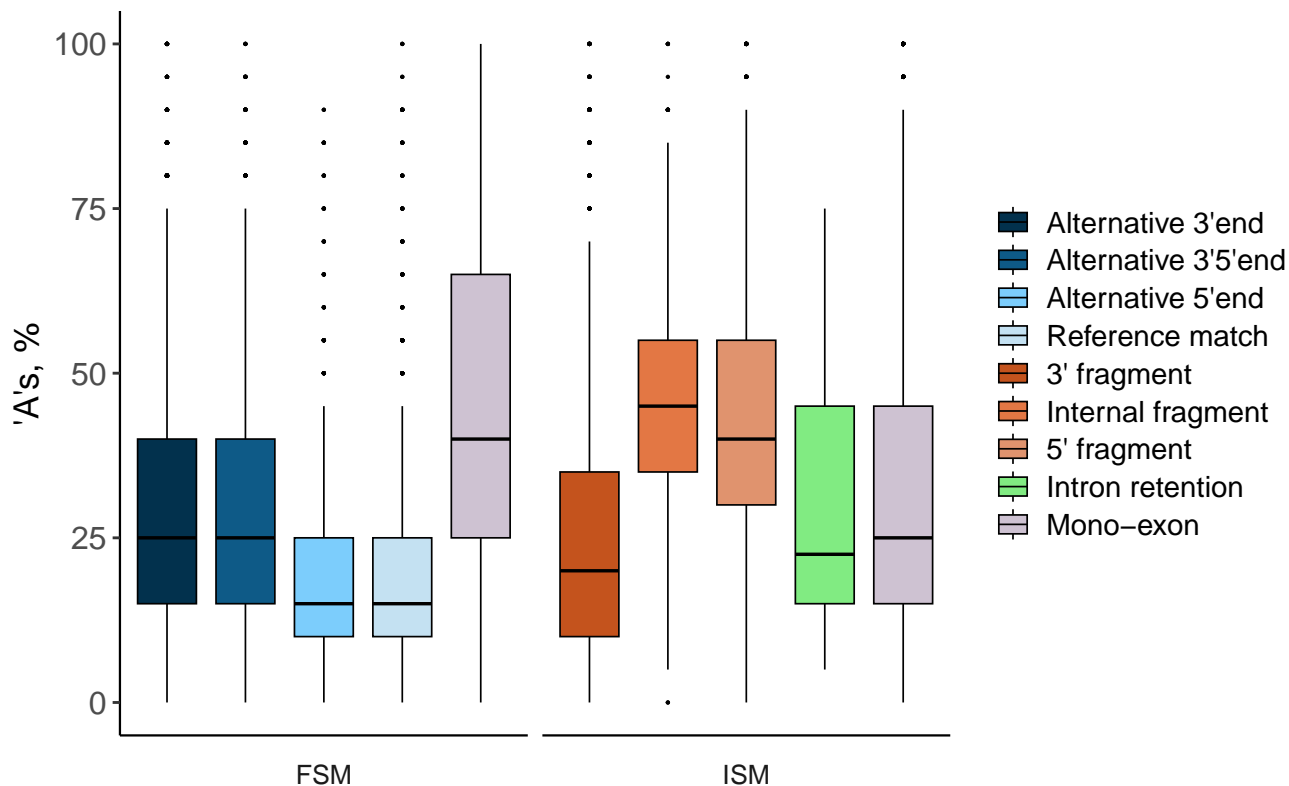
Reference Transcript Redundancy



Intra-Priming Quality Check

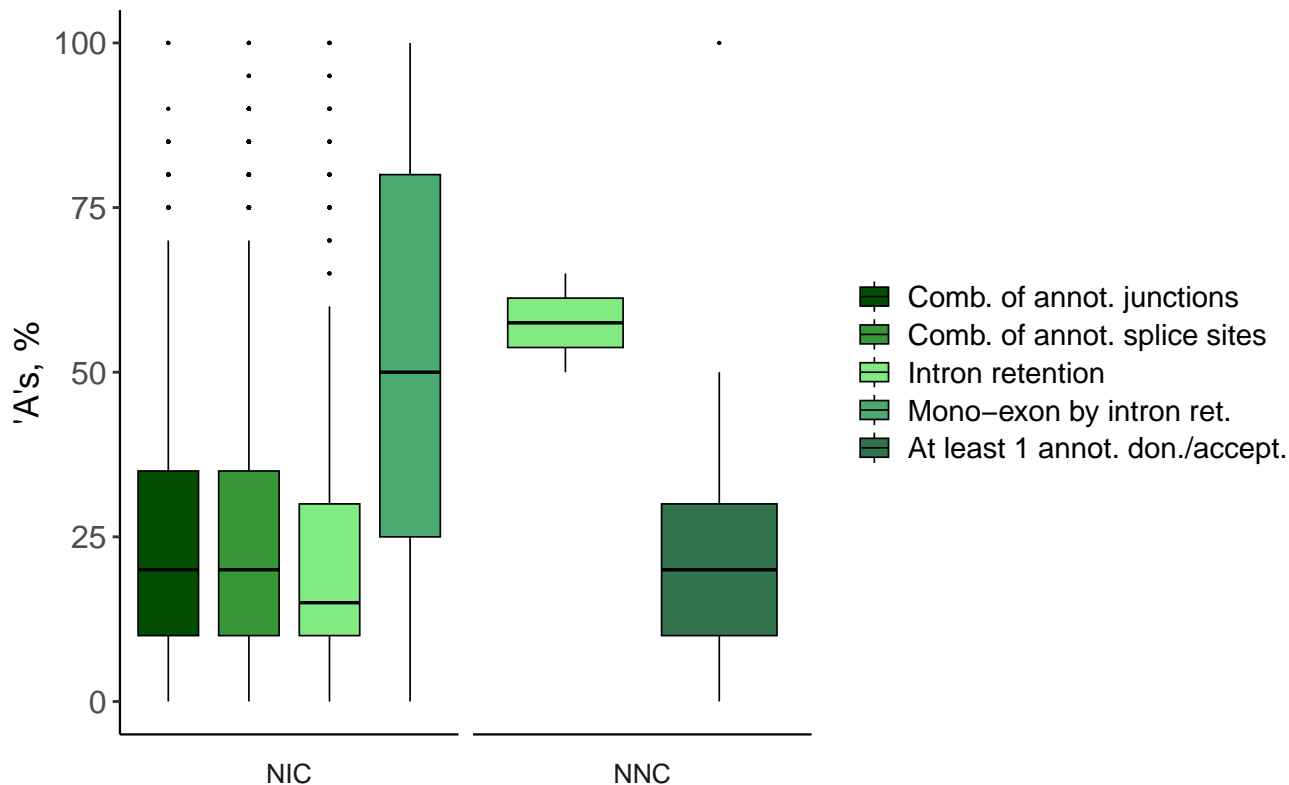
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



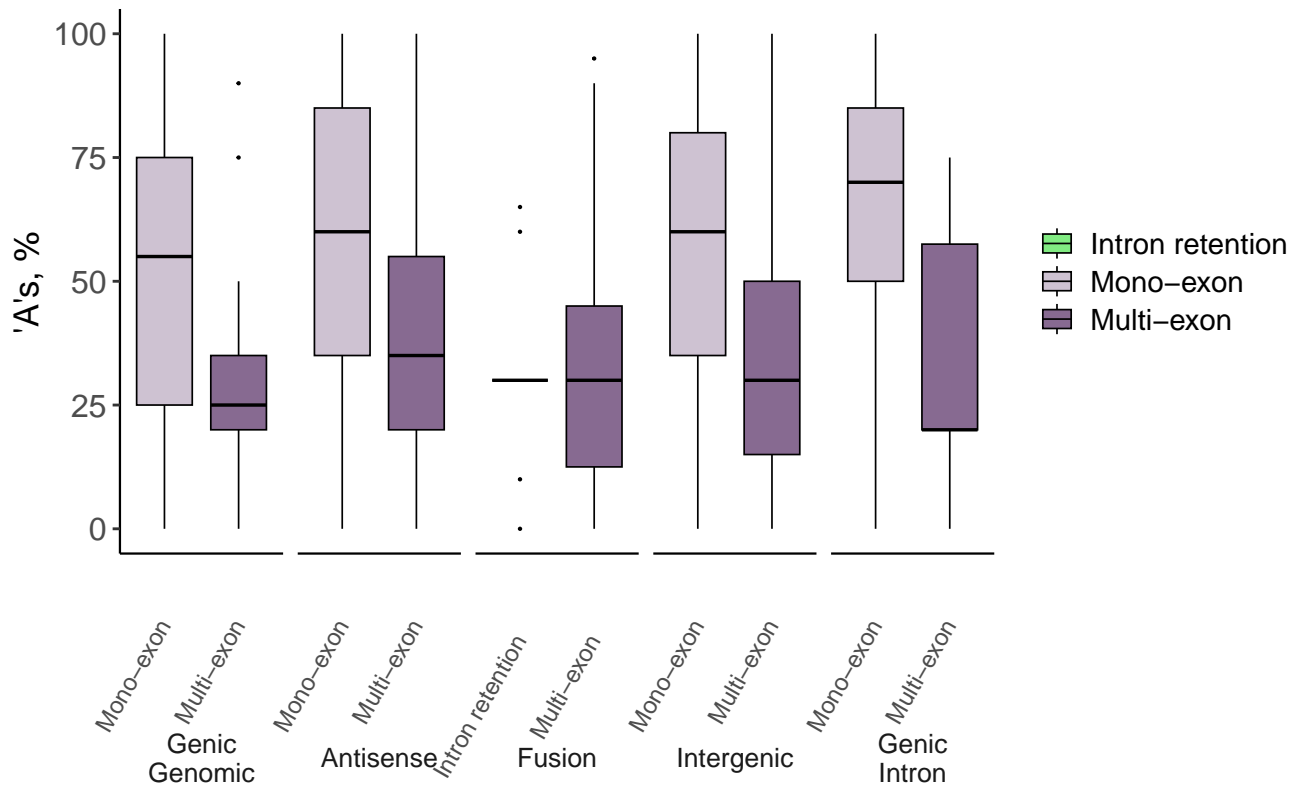
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



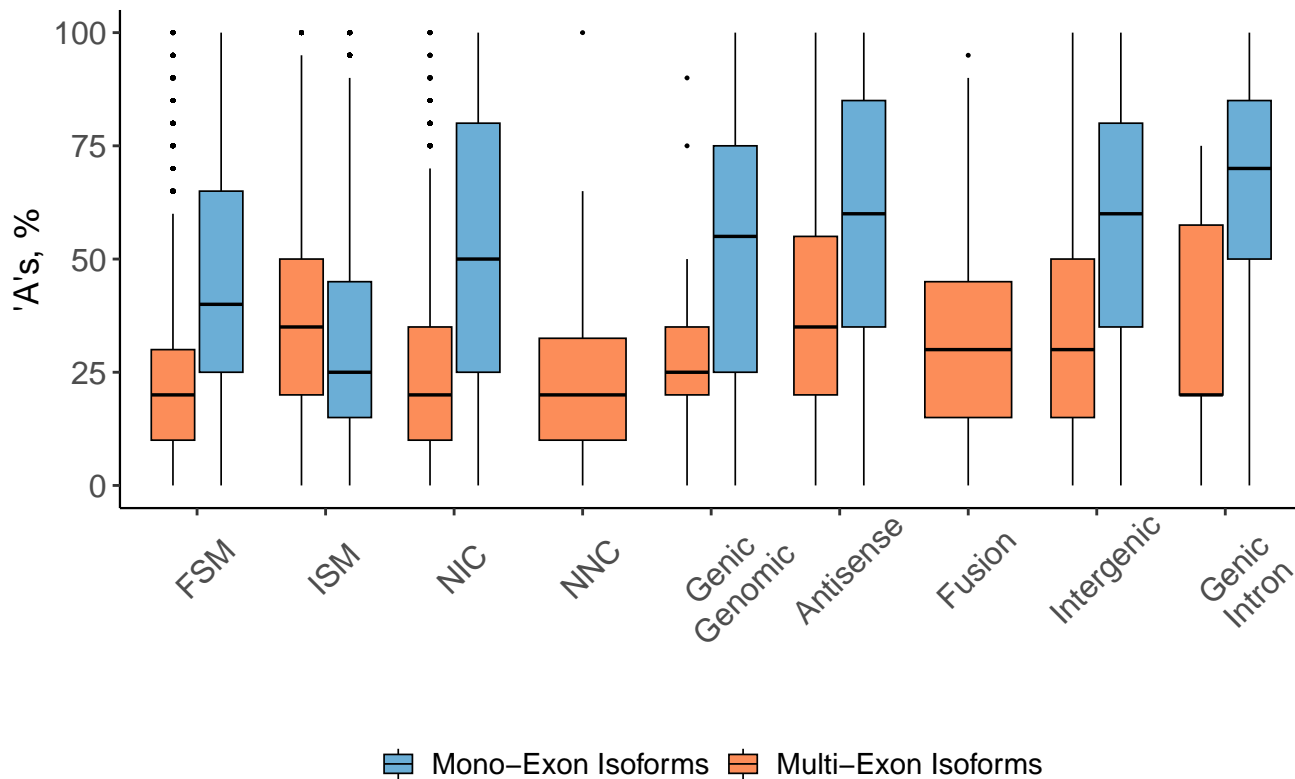
Possible Intra-Priming by Structural Category

Percent of genomic 'A's in downstream 20 bp



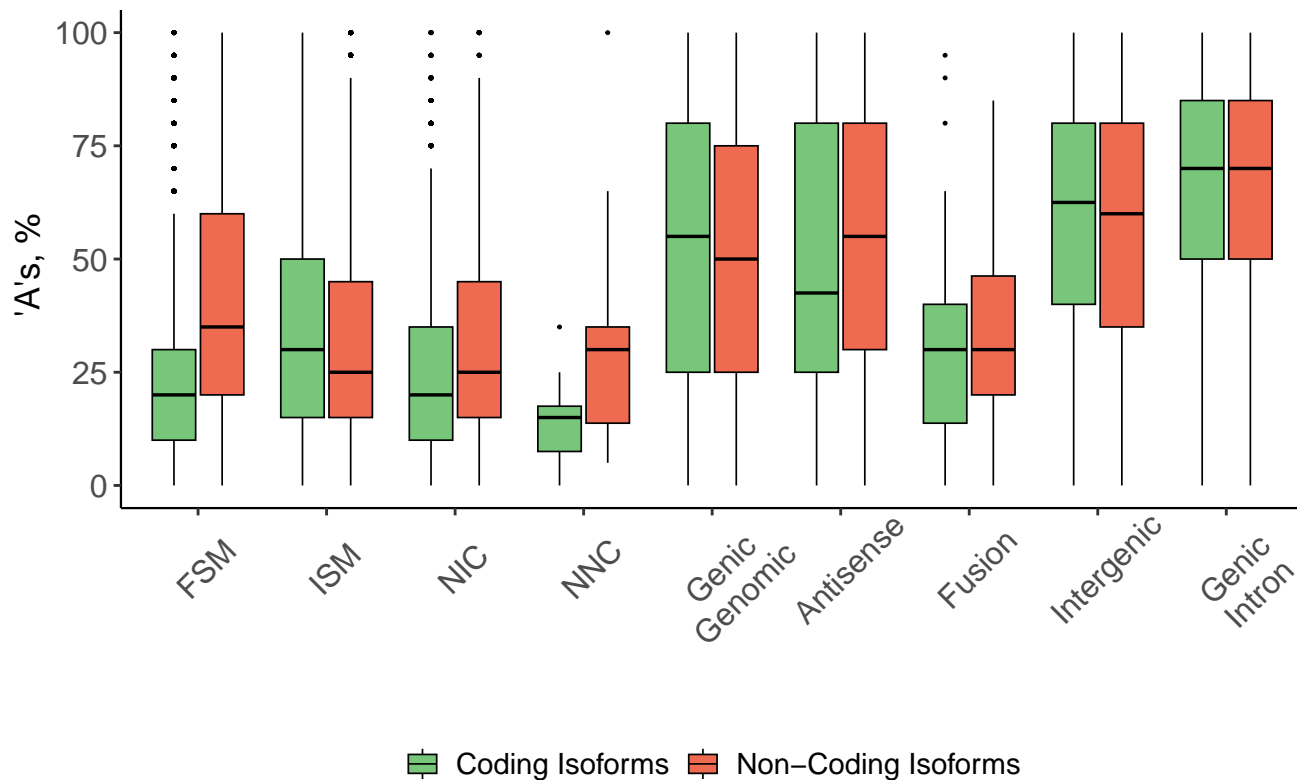
Mono- vs Multi-Exon Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp



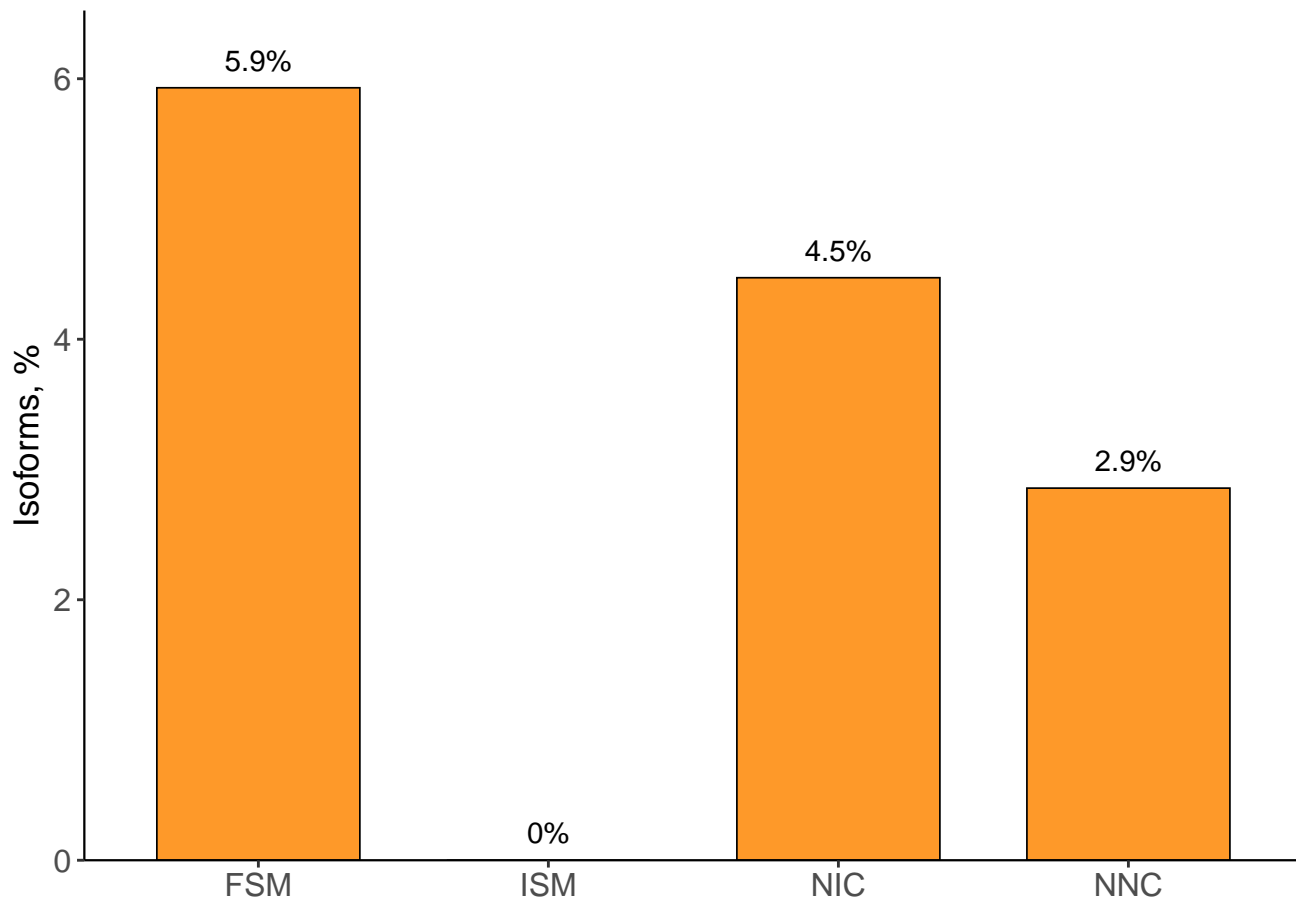
Coding vs Non-Coding Possible Intra-Priming

Percent of genomic 'A's in downstream 20 bp

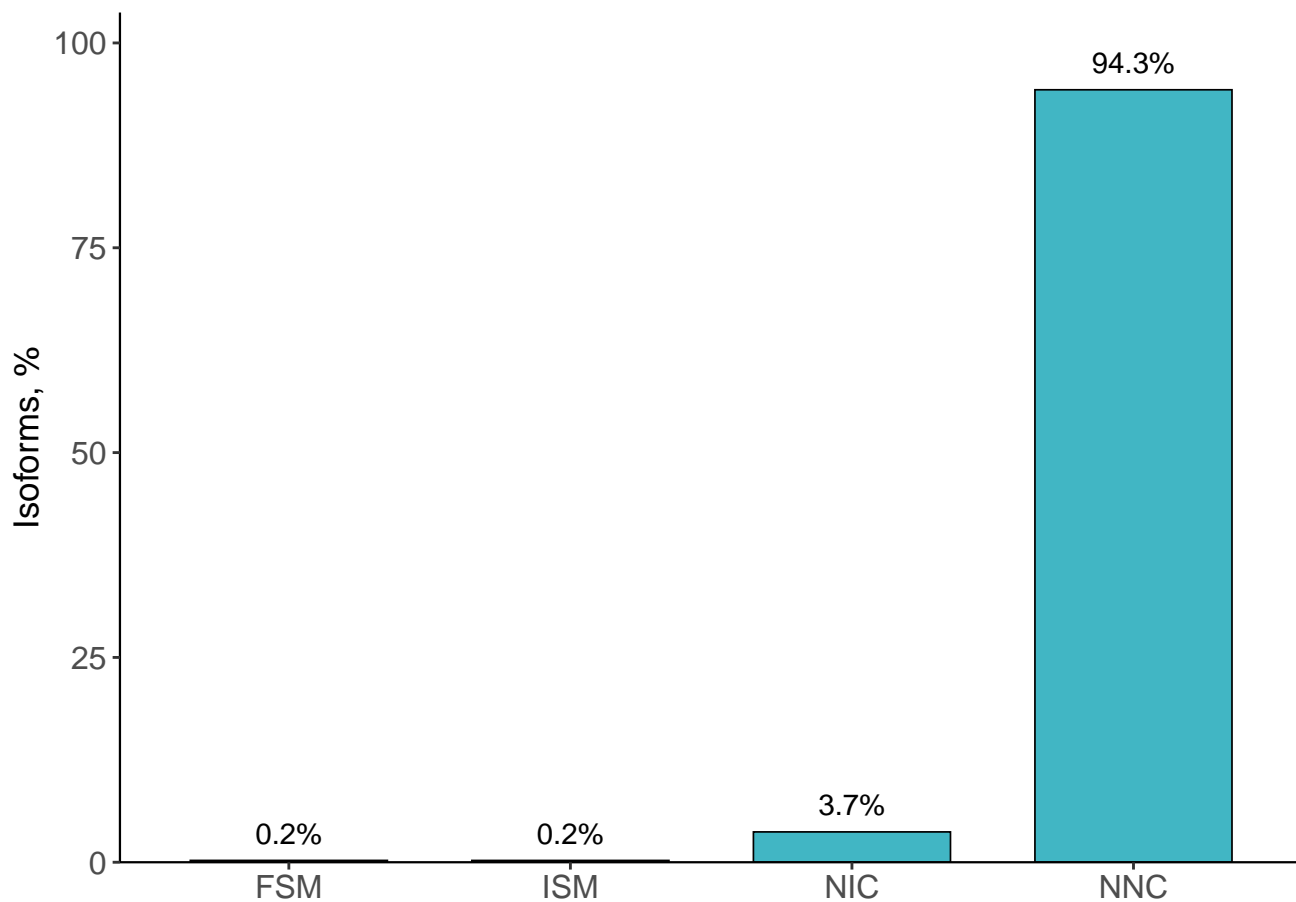


Features of Bad Quality

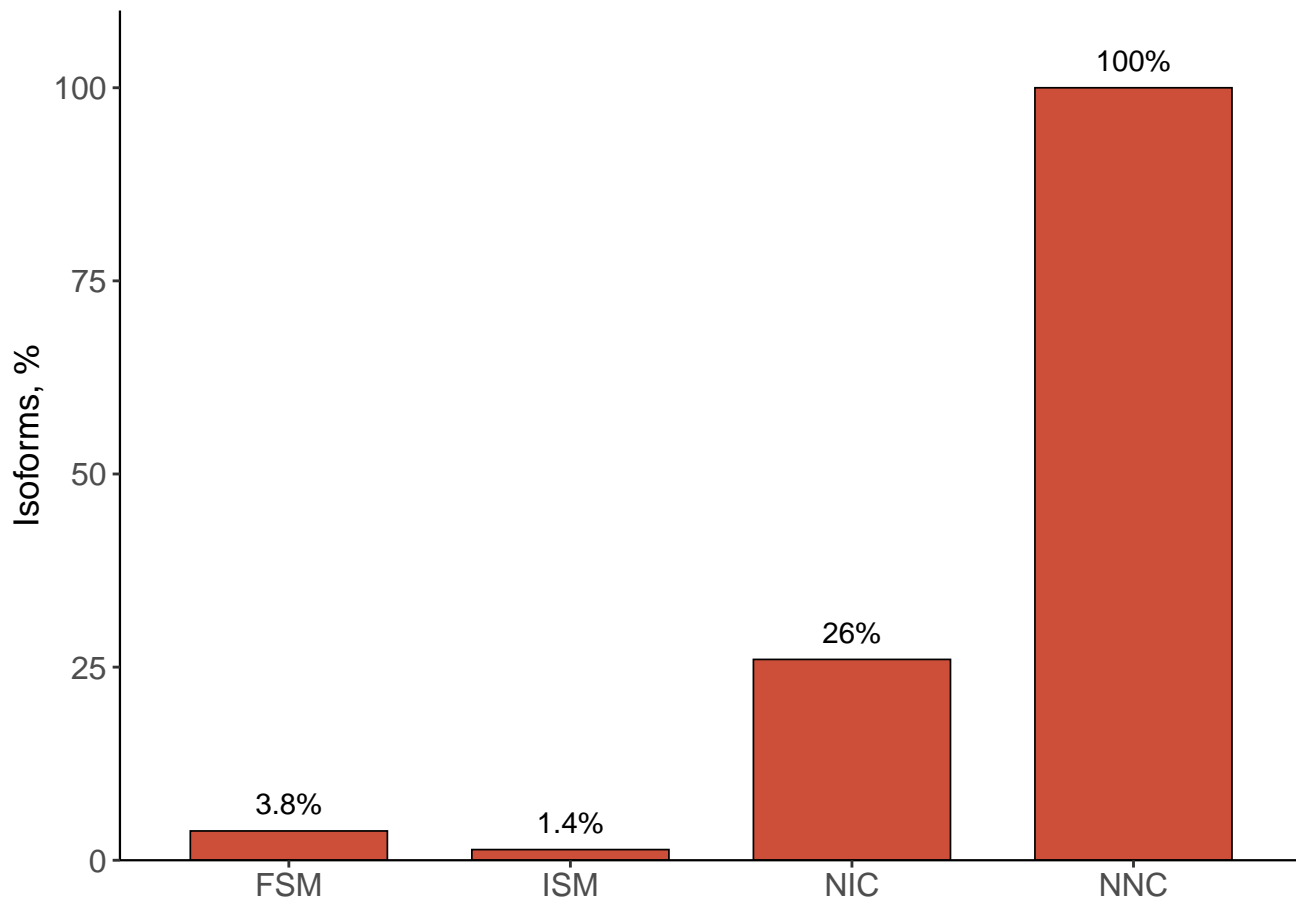
RT-switching



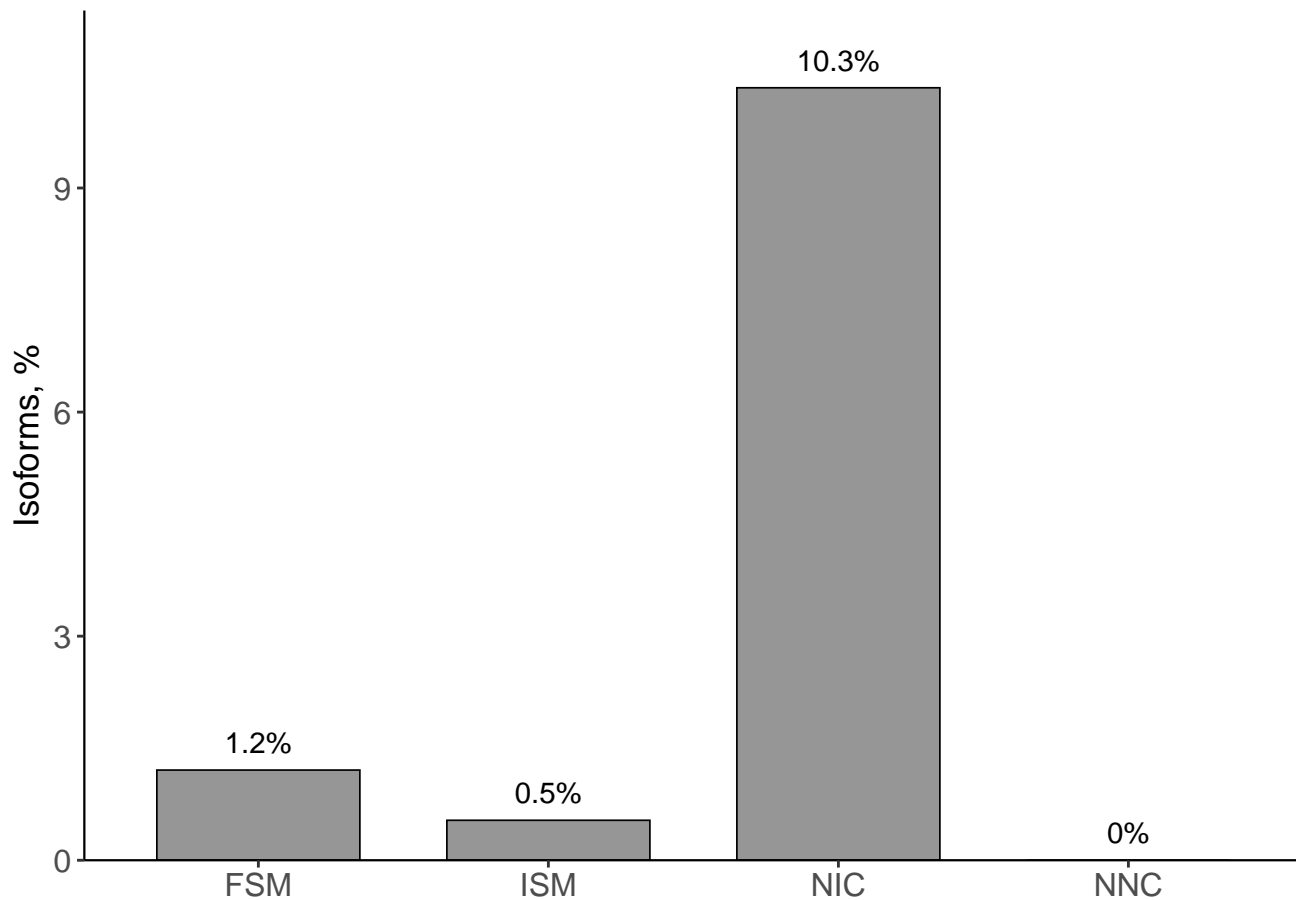
Non-Canonical Junctions



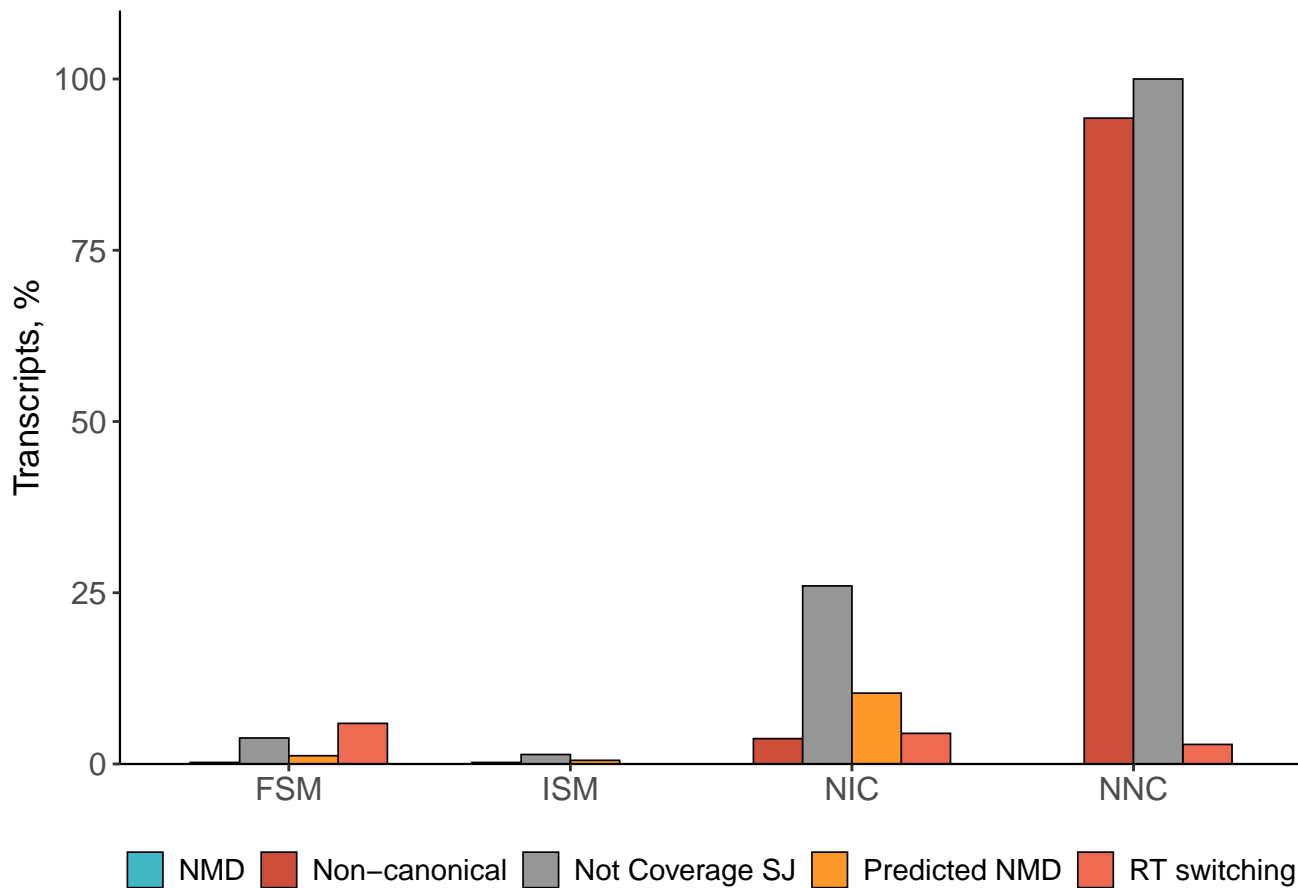
Splice Junctions Without Short Read Coverage



Nonsense-Mediated Decay by Structural Category

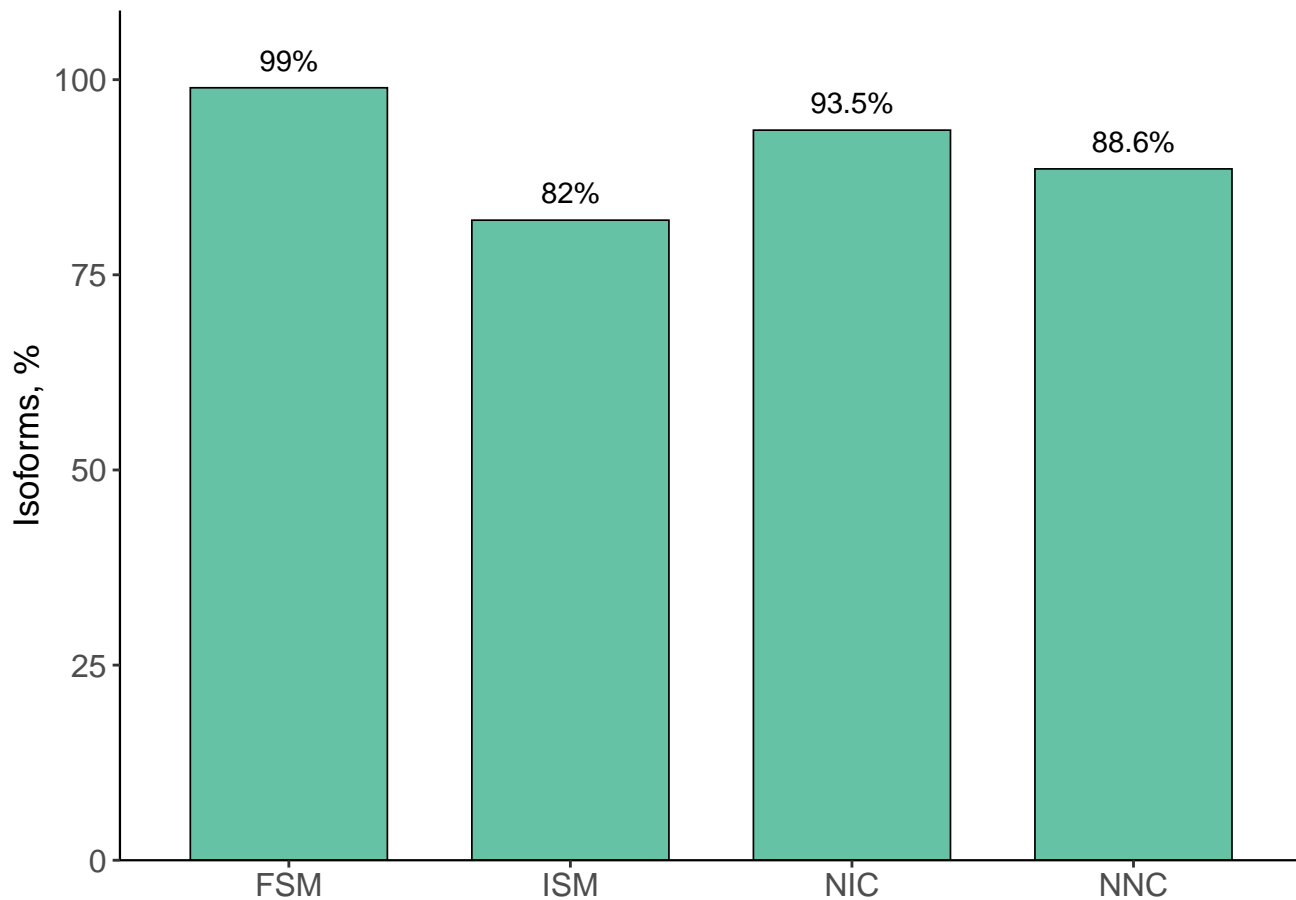


Quality Control Attributes Across Structural Categories

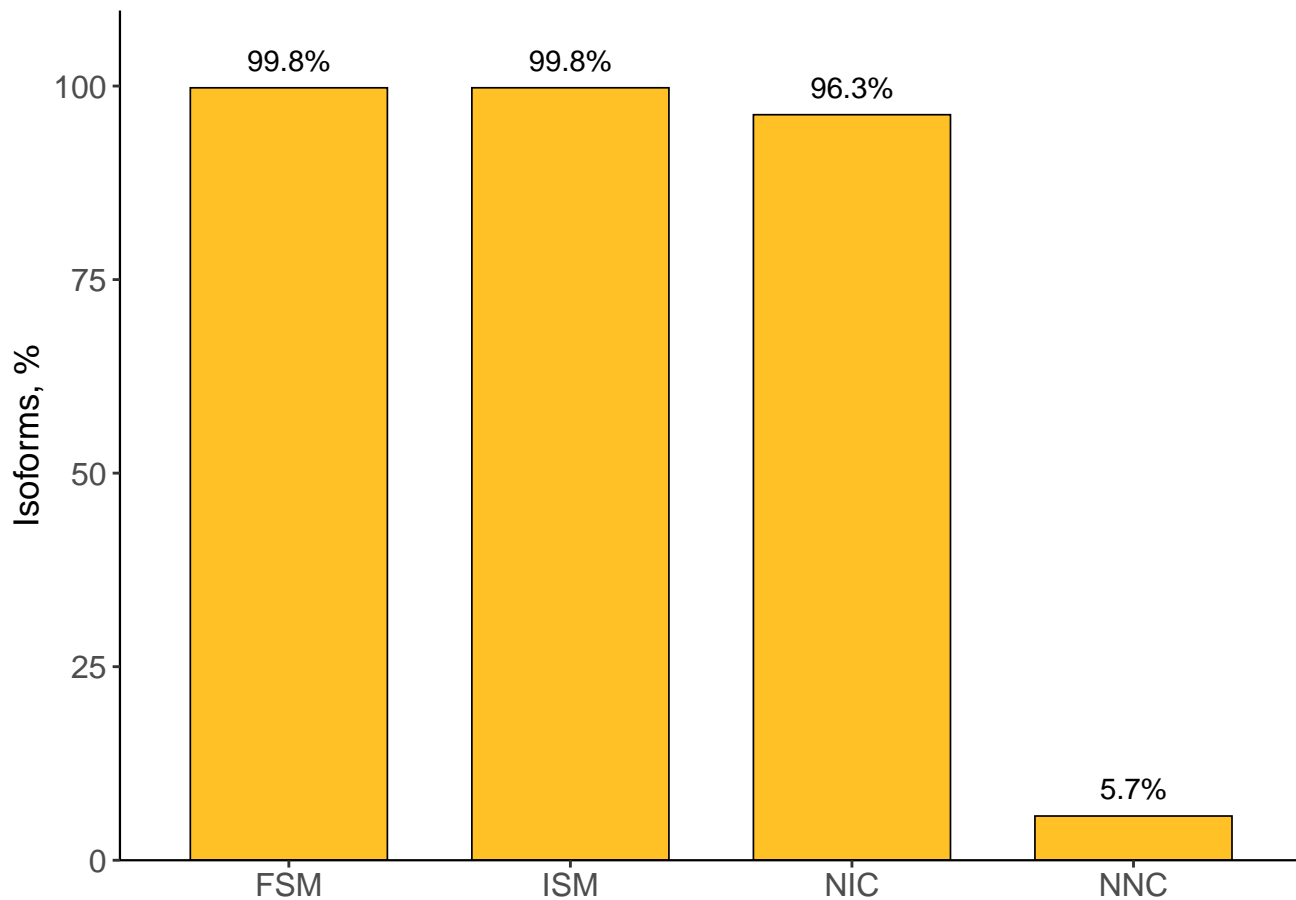


Features of Good Quality

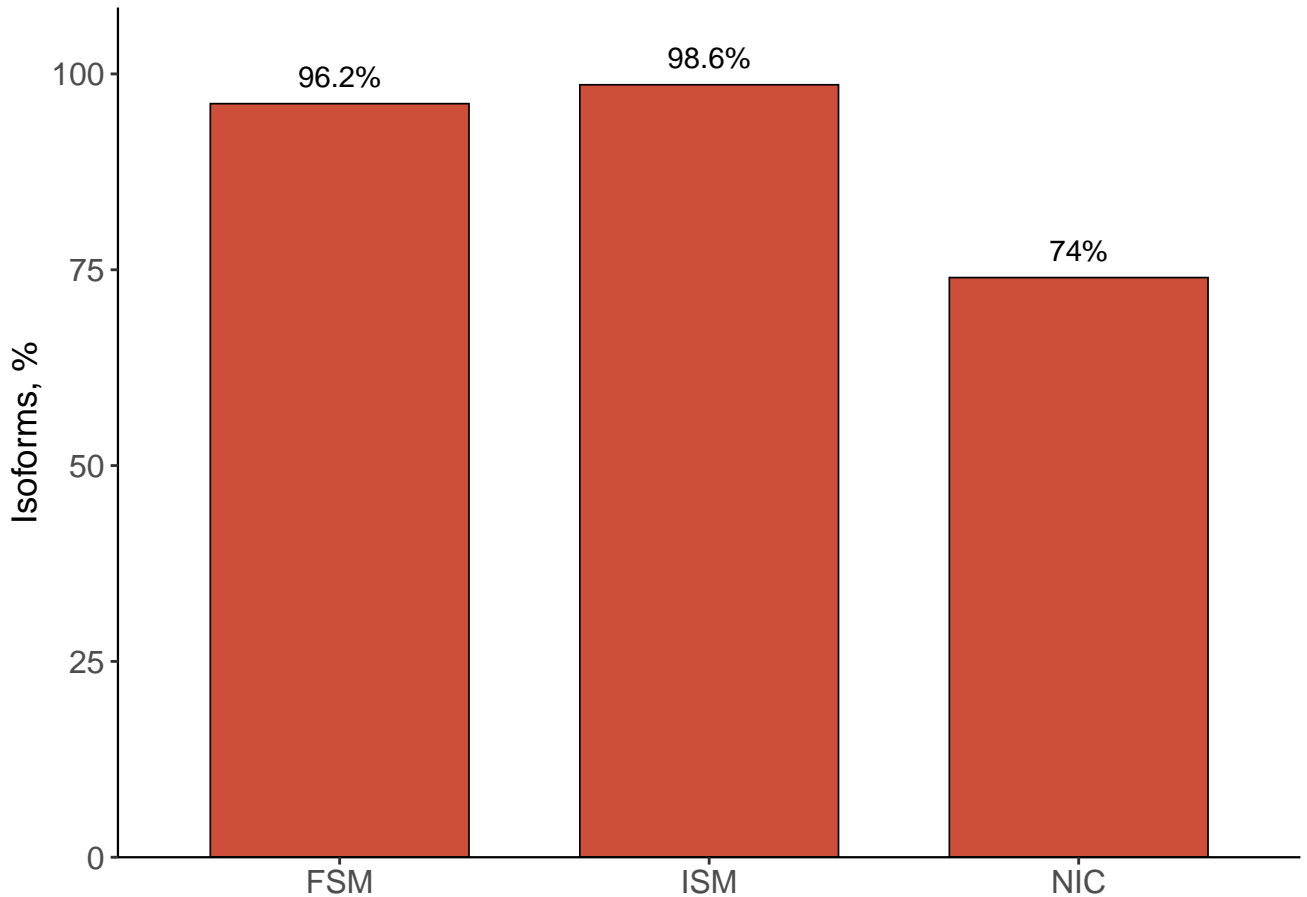
Annotation Support



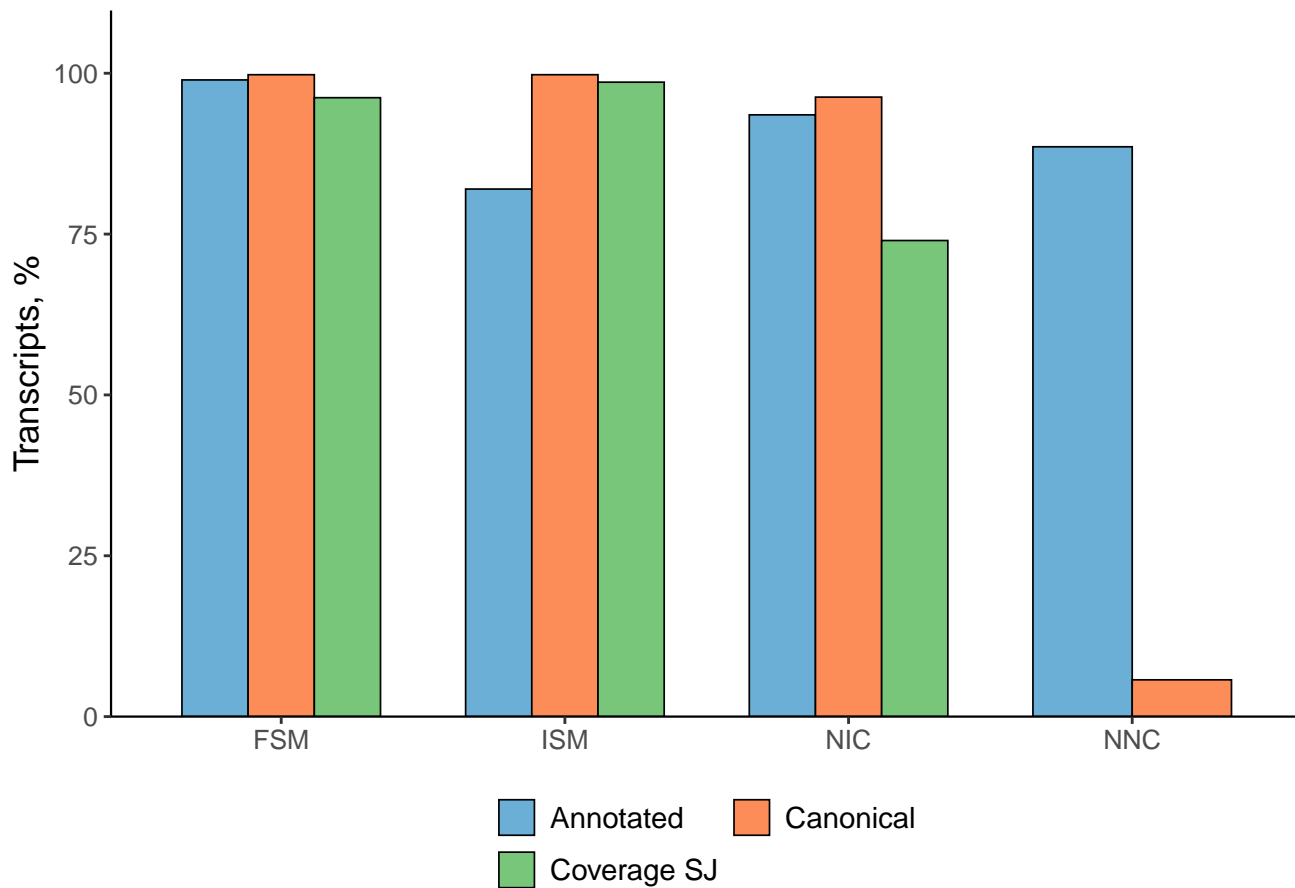
All Canonical Junctions



Splice Junctions With Short Read Coverage



Good Quality Control Attributes Across Structural Categories



TSS Ratio FSM Reference Match vs ISM

